

SEQUENCE LISTING

<110> Korneluk, Robert G.
Mackenzie, Alexander E.
Baird, Stephen
Liston, Peter

<120> MAMMALIAN IAP GENE FAMILY, PRIMERS,
PROBES, AND DETECTION METHODS

<130> 07891/003005

<150> 08/576,956

<151> 1995-12-22

<150> 08/511,485

<151> 1995-08-04

<160> 92

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 46

<212> PRT

<213> artificial sequence based on Homo sapiens, Mus musculus, Cydia pomonella, Orgyia pseudotsugata, and Drosophila melanogaster.

<220>

<221> VARIANT

<222> 8

<223> Glu or Asp

<221> VARIANT

<222> 14,22

<223> Val or Ile

<221> VARIANT

<222> (1)...(46)

<223> Xaa = Any Amino Acid

<400> 1

Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Lys	Xaa	Cys	Met
1				5					10						15	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Pro	Cys	Gly	His	Xaa	Xaa	Xaa	
			20					25					30			
Cys	Xaa	Xaa	Cys	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Pro	Xaa	Cys			
		35					40					45				

<210> 2
 <211> 68
 <212> PRT
 <213> artificial sequence based on Homo sapiens, Mus musculus, Cydia pomonella, Orgyia pseudotsugata, and Drosophila melanogaster.

<220>
 <221> VARIANT
 <222> 13,16,17
 <223> any amino acid or absent

<221> VARIANT
 <222> (1)...(68)
 <223> Xaa = Any Amino Acid

<400> 2
 Xaa Xaa Xaa Arg Leu Xaa Thr Phe Xaa Xaa Trp Pro Xaa Xaa Xaa Xaa
 1 5 10 15
 Xaa Xaa Xaa Xaa Xaa Leu Ala Xaa Ala Gly Phe Tyr Tyr Xaa Gly Xaa
 20 25 30
 Xaa Asp Xaa Val Xaa Cys Phe Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp
 35 40 45
 Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Pro Xaa
 50 55 60
 Cys Xaa Phe Val
 65

26/68

<210> 3
 <211> 2540
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)...(2540)
 <223> n = A,T,C, or G

<400> 3
 gaaaagggtgg acaagtccta ttttcaagag aagatgactt ttaacagttt tgaaggatct 60
 aaaacttggtg tacctgcaga catcaataag gaagaagaat ttgtagaaga gtttaataga 120
 ttaaaaaactt ttgctaattt tccaagtggg agtcctgttt cagcatcaac actggcacga 180
 gcagggtttc ttatactagg tgaaggagat accgtgctgg gcttttagttg tcatgcagct 240
 gtagatagat ggcaatatgg agactcagca gttggaagac acaggaaagt atccccaaat 300
 tgcagattta tcaacggcctt ttatcttgaa aatagtgcc aagcagctctac aaattctggt 360
 atccagaatg gtcagtacaa agttgaaaac tatctgggaa gcagagatca ttttgcctta 420
 gacaggccat ctgagacaca tgcagactat cttttgagaa ctgggcagggt tgtagatata 480
 tcagacacca tatacccgag gaaccctgcc atgtattgtg aagaagctag attaaagtcc 540
 tttcagaact ggccagacta tgctcaccta accccaagag agttagcaag tgctggactc 600
 tactacacag gtattggtga ccaagtgcag tgctttgtgt gtggtggaaa actgaaaaat 660
 tgggaacctt gtgatcgtgc ctgggtcagaa cacaggcgac actttcctaa ttgcttcttt 720
 gttttgggcc ggaatcttaa tattcgaagt gaatctgatg ctgtgagttc tgataggaat 780
 ttcccaaatt caacaaatct tccaagaaat ccatccatgg cagattatga agcacggatc 840

```

tttacttttg ggacatggat atactcagtt aacaaggagc agcttgcaag agctggattt 900
tatgcttttag gtgaagggtga taaagtaaag tgcttttact gtggaggagg gctaactgat 960
tggaagccca gtgaagaccc ttgggaacaa catgctaaat ggtatccagg gtgcaaatat 1020
ctgttagaac agaagggaca agaatatata aacaatattc atttaactca ttcacttgag 1080
gagtgtctgg taagaactac tgagaaaaaca ccatcactaa ctagaagaat tgatgatacc 1140
atcttccaaa atcctatggt acaagaagct atacgaatgg gggttcagttt caaggacatt 1200
aagaaaaataa tggaggaaaa aattcagata tctgggagca actataaatc acttgagggtt 1260
ctggttgcag atctagtga tgcacagaaa gacagtatgc aagatgagtc aagtcagact 1320
tcattacaga aagagattag tactgaagag cagctaaggc gcctgcaaga ggagaagctt 1380
tgcaaaatct gtatggatag aaatattgct atcgtttttg ttccttgtgg acatctagtc 1440
acttgtaaac aatgtgctga agcagttgac aagtgtccca tgtgctacac agtcattact 1500
ttcaagcaaa aaatttttat gtcttaatct aactctatag taggcatgtt atgttgttct 1560
tattaccctg attgaatgtg tgatgtgaac tgactttaag taatcaggat tgaattccat 1620
tagcatttgc taccaagtag gaaaaaaaat gtacatggca gtgttttagt tggcaatata 1680
atctttgaat ttcttgattt ttcaggggat tagctgtatt atccattttt tttactgtta 1740
tttaattgaa accatagact aagaataaga agcatcatac tataactgaa cacaatgtgt 1800
attcatagta tactgattta atttctaagt gtaagtgaat taatcatctg gattttttat 1860
tcttttcaga taggcttaac aaatggagct ttctgtatat aaatgtggag attagagtta 1920
atctcccca tccacataatt tgttttgtgt gaaaaaggaa taaattgttc catgctgggtg 1980
gaaagataga gattgttttt agaggttggg tgttgtgttt taggattctg tccattttct 2040
tgtaaaggga taaacacgga cgtgtgcgaa atatgtttgt aaagtgattt gccattgttg 2100
aaagcgtatt taatgataga atactatcga gccaacatgt actgacatgg aaagatgtca 2160
gagatatgtt aagtgtaaaa tgcaagtggc gggacactat gtatagtctg agccagatca 2220
aagtatgtat gttgttaata tgcatagaac gagagatttg gaaagatata caccaaactg 2280
ttaaatgtgg tttctcttcg gggagggggg gattggggga ggggccccag aggggtttta 2340
gaggggcctt ttcacttttcg acttttttca ttttgttctg ttcggatttt ttataagtat 2400
gtagaccccc aagggtttta tgggaactaa catcagtaac ctaacccccg tgactatcct 2460
gtgctcttcc tagggagctg tgttgtttcc caccaccac ccttccctct gaacaaatgc 2520
ctgagtgtctg gggcactttt 2540

```

<210> 4
 <211> 497
 <212> PRT
 <213> Homo sapiens

<400> 4

Met	Thr	Phe	Asn	Ser	Phe	Glu	Gly	Ser	Lys	Thr	Cys	Val	Pro	Ala	Asp
1			5					10						15	
Ile	Asn	Lys	Glu	Glu	Glu	Phe	Val	Glu	Glu	Phe	Asn	Arg	Leu	Lys	Thr
		20						25					30		
Phe	Ala	Asn	Phe	Pro	Ser	Gly	Ser	Pro	Val	Ser	Ala	Ser	Thr	Leu	Ala
		35				40					45				
Arg	Ala	Gly	Phe	Leu	Tyr	Thr	Gly	Glu	Gly	Asp	Thr	Val	Arg	Cys	Phe
		50				55					60				
Ser	Cys	His	Ala	Ala	Val	Asp	Arg	Trp	Gln	Tyr	Gly	Asp	Ser	Ala	Val
		65			70				75					80	
Gly	Arg	His	Arg	Lys	Val	Ser	Pro	Asn	Cys	Arg	Phe	Ile	Asn	Gly	Phe
		85						90					95		
Tyr	Leu	Glu	Asn	Ser	Ala	Thr	Gln	Ser	Thr	Asn	Ser	Gly	Ile	Gln	Asn
		100						105					110		
Gly	Gln	Tyr	Lys	Val	Glu	Asn	Tyr	Leu	Gly	Ser	Arg	Asp	His	Phe	Ala
		115				120						125			
Leu	Asp	Arg	Pro	Ser	Glu	Thr	His	Ala	Asp	Tyr	Leu	Leu	Arg	Thr	Gly
		130				135					140				

Gln	Val	Val	Asp	Ile	Ser	Asp	Thr	Ile	Tyr	Pro	Arg	Asn	Pro	Ala	Met
145					150					155					160
Tyr	Cys	Glu	Glu	Ala	Arg	Leu	Lys	Ser	Phe	Gln	Asn	Trp	Pro	Asp	Tyr
				165					170					175	
Ala	His	Leu	Thr	Pro	Arg	Glu	Leu	Ala	Ser	Ala	Gly	Leu	Tyr	Tyr	Thr
			180					185					190		
Gly	Ile	Gly	Asp	Gln	Val	Gln	Cys	Phe	Cys	Cys	Gly	Gly	Lys	Leu	Lys
		195					200					205			
Asn	Trp	Glu	Pro	Cys	Asp	Arg	Ala	Trp	Ser	Glu	His	Arg	Arg	His	Phe
210						215					220				
Pro	Asn	Cys	Phe	Phe	Val	Leu	Gly	Arg	Asn	Leu	Asn	Ile	Arg	Ser	Glu
225					230					235					240
Ser	Asp	Ala	Val	Ser	Ser	Asp	Arg	Asn	Phe	Pro	Asn	Ser	Thr	Asn	Leu
			245						250					255	
Pro	Arg	Asn	Pro	Ser	Met	Ala	Asp	Tyr	Glu	Ala	Arg	Ile	Phe	Thr	Phe
		260						265					270		
Gly	Thr	Trp	Ile	Tyr	Ser	Val	Asn	Lys	Glu	Gln	Leu	Ala	Arg	Ala	Gly
		275					280					285			
Phe	Tyr	Ala	Leu	Gly	Glu	Gly	Asp	Lys	Val	Lys	Cys	Phe	His	Cys	Gly
290						295				300					
Gly	Gly	Leu	Thr	Asp	Trp	Lys	Pro	Ser	Glu	Asp	Pro	Trp	Glu	Gln	His
305					310					315					320
Ala	Lys	Trp	Tyr	Pro	Gly	Cys	Lys	Tyr	Leu	Leu	Glu	Gln	Lys	Gly	Gln
			325						330					335	
Glu	Tyr	Ile	Asn	Asn	Ile	His	Leu	Thr	His	Ser	Leu	Glu	Glu	Cys	Leu
		340					345					350			
Val	Arg	Thr	Thr	Glu	Lys	Thr	Pro	Ser	Leu	Thr	Arg	Arg	Ile	Asp	Asp
		355					360					365			
Thr	Ile	Phe	Gln	Asn	Pro	Met	Val	Gln	Glu	Ala	Ile	Arg	Met	Gly	Phe
370						375					380				
Ser	Phe	Lys	Asp	Ile	Lys	Lys	Ile	Met	Glu	Glu	Lys	Ile	Gln	Ile	Ser
385					390					395					400
Gly	Ser	Asn	Tyr	Lys	Ser	Leu	Glu	Val	Leu	Val	Ala	Asp	Leu	Val	Asn
			405						410					415	
Ala	Gln	Lys	Asp	Ser	Met	Gln	Asp	Glu	Ser	Ser	Gln	Thr	Ser	Leu	Gln
			420					425					430		
Lys	Glu	Ile	Ser	Thr	Glu	Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Lys
		435					440					445			
Leu	Cys	Lys	Ile	Cys	Met	Asp	Arg	Asn	Ile	Ala	Ile	Val	Phe	Val	Pro
450						455				460					
Cys	Gly	His	Leu	Val	Thr	Cys	Lys	Gln	Cys	Ala	Glu	Ala	Val	Asp	Lys
465					470					475					480
Cys	Pro	Met	Cys	Tyr	Thr	Val	Ile	Thr	Phe	Lys	Gln	Lys	Ile	Phe	Met
			485						490					495	
Ser															

<210> 5
 <211> 2676
 <212> DNA
 <213> Homo sapiens

<220>
 <221> Variant
 <222> (1)...(2676)
 <223> n = A,T,C,or G

<400> 5
 tccttgagat gtatcagtat aggatttagg atctccatgt tggaactcta aatgcataga 60
 aatggaaata atggaaattt ttcatttttg cttttcagcc tagtattaaa actgataaaa 120
 gcaaagccat gcacaaaact acctccctag agaaaaggcta gtcccttttc ttccccattc 180
 atttcattat gaacatagta gaaaacagca tattcttatc aaatttgatg aaaagcgcca 240
 acacgtttga actgaaatac gacttgatcat gtgaactgta ccgaatgtct acgtattcca 300
 cttttcctgc tgggggttct gtctcagaaa ggagtccttc tcgtgctggg ttctattaca 360
 ctgggtgtgaa tgacaagggtc aaatgccttc gttgtggcct gatgctggat aactggaaaa 420
 gaggagacag tcctactgaa aagcataaaa agttgtatcc tagctgcaga ttcgttcaga 480
 gtctaaattc cgtaacaac ttggaagcta cctctcagcc tacttttctc tcttcagtaa 540
 cacattccac acactcatta cttccgggta cagaaaacag tggatatttc cgtggctctt 600
 attcaaactc tccatcaaat cctgtaaaact ccagagcaaa tcaagaattt tctgccttga 660
 tgagaagttc ctacccctgt ccaatgaata acgaaaatgc cagattactt acttttcaga 720
 catggccatt gacttttctg tcgccaacag atctggcacg agcaggcttt tactacatag 780
 gacctggaga cagagtggct tgctttgcct gtgggtggaaa attgagcaat tgggaaccga 840
 aggataatgc tatgtcagaa cacctgagac attttcccaa atgcccattt atagaaaatc 900
 agcttcaaga cacttcaaga tacacagttt ctaatctgag catgcagaca catgcagccc 960
 gctttaaaac attctttaac tggccctcta gtgttctagt taatcctgag cagcttgcaa 1020
 gtgcgggttt ttattatgtg ggtaacagtg atgatgtcaa atgcttttgc tgtgatgggtg 1080
 gactcagggtg ttgggaatct ggagatgatc catgggttca acatgccaag tggtttccaa 1140
 ggtgtgagta cttgataaga attaaaggac aggagtcat ccgtcaagtt caagccagtt 1200
 accctcatct acttgaacag ctgctatcca catcagacag cccaggagat gaaaatgcag 1260
 agtcatcaat tatccatttg gaacctggag aagaccattc agaagatgca atcatgatga 1320
 atactcctgt gattaatgct gccgtggaaa tgggctttag tagaagcctg gtaaaacaga 1380
 cagttcagag aaaaatccta gcaactggag agaattatag actagtcaat gatcttgtgt 1440
 tagacttact caatgcagaa gatgaaataa gggaagagga gagagaaaga gcaactgagg 1500
 aaaaagaatc aaatgattta ttattaatcc ggaagaatag aatggcactt tttcaacatt 1560
 tgacttgtgt aattccaatc ctggatagtc tactaactgc cggaattatt aatgaacaag 1620
 aacatgtatg tattaacacg aagacacaga cgtctttaca agcaagagaa ctgattgata 1680
 cagttttagt aaaaggaaat attgcagcca ctgtattcag aaactctctg caagaagctg 1740
 aagctgtgtt atatgagcat ttatttgtgc aacaggacat aaaatatatt cccacagaag 1800
 atgtttcaga tctaccagtg gaagaacaat tgcggagact accagaagaa agaacatgta 1860
 aagtgtgtat ggacaaagaa gtgtccatag tgtttatttc ttgtgggtcat ctagtagtat 1920
 gcaaagattg tgctccttct ttaagaaagt gtctattttg taggagtaca atcaagggtg 1980
 cagttcgtac atttctttca tgaagaagaa ccaaaacatc gtctaaactt tagaattaat 2040
 ttattaaatg tattataact ttaactttta tcctaatttg gtttccttaa aatttttatt 2100
 tattttacaac tcaaaaaaca ttgttttgtg taacatattt atatatgtat ctaaaccata 2160
 tgaacatata ttttttagaa actaagagaa tgataggctt ttgttcttat gaacgaaaaa 2220
 gaggtagcac tacaaacaca atattcaatc caaatttcag cattattgaa attgtaagtg 2280
 aagtaaaaact taagatattt gagttaacct ttaagaattt taaatatttt ggcatgtac 2340
 taataccggg aacatgaagc cagggtgtggg ggtatgtacc tgtagtccca ggctgaggca 2400
 agagaattac ttgagcccag gagtttgaat ccactctggg cagcactactg agacctgcc 2460
 tttaaaaacn aacagnacca aanccaaaca ccagggacac atttctctgt cttttttgat 2520
 cagtgtccta tacatcgaag gtgtgcatat atgttgaatc acatttttagg gacatgggtg 2580
 ttttataaag aattctgtga gnaaaaattt aataaagcaa ccaaattact cttaaaaaaa 2640
 aaaaaaaaaa aaaaaactcg aggggcccggt accaat 2676

00654743-090100

<210> 6
 <211> 604
 <212> PRT
 <213> Homo sapiens

<400> 6
 Met Asn Ile Val Glu Asn Ser Ile Phe Leu Ser Asn Leu Met Lys Ser
 1 5 10 15
 Ala Asn Thr Phe Glu Leu Lys Tyr Asp Leu Ser Cys Glu Leu Tyr Arg
 20 25 30
 Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu Arg
 35 40 45
 Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys Val
 50 55 60
 Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Arg Gly Asp
 65 70 75 80
 Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser Cys Arg Phe Val
 85 90 95
 Gln Ser Leu Asn Ser Val Asn Asn Leu Glu Ala Thr Ser Gln Pro Thr
 100 105 110
 Phe Pro Ser Ser Val Thr His Ser Thr His Ser Leu Leu Pro Gly Thr
 115 120 125
 Glu Asn Ser Gly Tyr Phe Arg Gly Ser Tyr Ser Asn Ser Pro Ser Asn
 130 135 140
 Pro Val Asn Ser Arg Ala Asn Gln Glu Phe Ser Ala Leu Met Arg Ser
 145 150 155 160
 Ser Tyr Pro Cys Pro Met Asn Asn Glu Asn Ala Arg Leu Leu Thr Phe
 165 170 175
 Gln Thr Trp Pro Leu Thr Phe Leu Ser Pro Thr Asp Leu Ala Arg Ala
 180 185 190
 Gly Phe Tyr Tyr Ile Gly Pro Gly Asp Arg Val Ala Cys Phe Ala Cys
 195 200 205
 Gly Gly Lys Leu Ser Asn Trp Glu Pro Lys Asp Asn Ala Met Ser Glu
 210 215 220
 His Leu Arg His Phe Pro Lys Cys Pro Phe Ile Glu Asn Gln Leu Gln
 225 230 235 240
 Asp Thr Ser Arg Tyr Thr Val Ser Asn Leu Ser Met Gln Thr His Ala
 245 250 255
 Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu Val Asn
 260 265 270
 Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
 275 280 285
 Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
 290 295 300
 Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
 305 310 315 320
 Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val Gln Ala
 325 330 335
 Ser Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Ser Pro
 340 345 350
 Gly Asp Glu Asn Ala Glu Ser Ser Ile Ile His Leu Glu Pro Gly Glu
 355 360 365

001060 "E34743" 090100

Asp	His	Ser	Glu	Asp	Ala	Ile	Met	Met	Asn	Thr	Pro	Val	Ile	Asn	Ala
370						375					380				
Ala	Val	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Lys	Gln	Thr	Val	Gln
385					390					395					400
Arg	Lys	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Leu	Val	Asn	Asp	Leu
				405					410					415	
Val	Leu	Asp	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Ile	Arg	Glu	Glu	Glu	Arg
			420					425					430		
Glu	Arg	Ala	Thr	Glu	Glu	Lys	Glu	Ser	Asn	Asp	Leu	Leu	Leu	Ile	Arg
		435					440					445			
Lys	Asn	Arg	Met	Ala	Leu	Phe	Gln	His	Leu	Thr	Cys	Val	Ile	Pro	Ile
	450					455					460				
Leu	Asp	Ser	Leu	Leu	Thr	Ala	Gly	Ile	Ile	Asn	Glu	Gln	Glu	His	Asp
465					470					475					480
Val	Ile	Lys	Gln	Lys	Thr	Gln	Thr	Ser	Leu	Gln	Ala	Arg	Glu	Leu	Ile
				485					490					495	
Asp	Thr	Ile	Leu	Val	Lys	Gly	Asn	Ile	Ala	Ala	Thr	Val	Phe	Arg	Asn
			500					505					510		
Ser	Leu	Gln	Glu	Ala	Glu	Ala	Val	Leu	Tyr	Glu	His	Leu	Phe	Val	Gln
		515					520					525			
Gln	Asp	Ile	Lys	Tyr	Ile	Pro	Thr	Glu	Asp	Val	Ser	Asp	Leu	Pro	Val
	530					535					540				
Glu	Glu	Gln	Leu	Arg	Arg	Leu	Pro	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys
545					550					555					560
Met	Asp	Lys	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val
				565					570					575	
Val	Cys	Lys	Asp	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys	Arg
			580					585					590		
Ser	Thr	Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser				
		595					600								

<210> 7

<211> 2580

<212> DNA

<213> Homo sapiens

<220>

<221> Variant

<222> (1) ... (2580)

<223> n = A,T,C,or G

<400> 7

```

ttaggttacc tgaaagagtt actacaaccc caaagagttg tgttctaagt agtatcttgg 60
taattcagag agatactcat cctacctgaa tataaactga gataaatcca gtaaagaaag 120
tgtagtaaag tctacataag agtctatcat tgatttcttt ttgtggtgga aatcttagtt 180
catgtgaaga aatttcatgt gaatgtttta gctatcaaac agtactgtca cctactcatg 240
cacaaaactg cctcccaaag acttttccca ggtccctcgt atcaaaacat taagagtata 300
atggaagata gcacgatctt gtcagattgg acaaacagca acaaacaaaa aatgaagtat 360
gacttttcct gtgaactcta cagaatgtct acatattcaa ctttccccgc cggggtgcct 420
gtctcagaaa ggagtcttgc tcgtgctggg ttttattata ctggtgtgaa tgacaaggtc 480
aaatgcttct gttgtggcct gatgctggat aactggaaac taggagacag tcctattcaa 540
aagcataaac agctatatcc tagctgtagc tttattcaga atctggtttc agctagtctg 600
ggatccacct ctaagaatac gtctccaatg agaaacagtt ttgcacattc attatctccc 660

```

```

accttgaac atagtagctt gttcagtgg tcttactcca gccttcctcc aaaccctctt 720
aattctagag cagttgaaga catctcttca tctgaggacta acccctacag ttatgcaatg 780
agtactgaag aagccagatt tcttacctac catatgtggc cattaacttt tttgtcacca 840
tcagaattgg caagagctgg tttttattat ataggacctg gagatagggg agcctgcttt 900
gcctgtgggtg ggaagctcag taactgggaa ccaaaggatg atgctatgtc agaacaccgg 960
-----
aggcattttc ccaactgtcc atttttggaa aattctctag aaactctgag gtttagcatt 1020
tcaaactctga gcatgcagac acatgcagct cgaatgagaa catttatgta ctggccatct 1080
agtgttccag ttcagcctga gcagcttgca agtgctgggt tttattatgt gggtcgcaat 1140
gatgatgtca aatgctttgg ttgtgatggg ggcttgaggt gttgggaatc tggagatgat 1200
ccatgggtag aacatgccaa gtggtttcca aggtgtgagt tcttgatacg aatgaaaggc 1260
caagagtttg ttgatgagat tcaaggtaga tatcctcatc ttcttgaaca gctgttgtca 1320
acttcagata ccactggaga agaaaatgct gaccaccaa ttattcattt tggacctgga 1380
gaaagtctct cagaagatgc tgtcatgatg aatacacctg tggttaaatc tgccttggaa 1440
atgggcttta atagagacct ggtgaaacaa acagttctaa gtaaaatcct gacaactgga 1500
gagaactata aaacagttaa tgatattgtg tcagcacttc ttaatgctga agatgaaaaa 1560
agagaagagg agaaggaaaa acaagctgaa gaaatggcat cagatgattt gtcattaatt 1620
cggaagaaca gaatggctct ctttcaacaa ttgacatgtg tgcttcctat cctggataat 1680
cttttaaagg ccaatgtaat taataaacag gaacatgata ttattaaaca aaaaacacag 1740
atacctttac aagcgagaga actgattgat accatttggg ttaaaggaaa tgctgcggcc 1800
aacatcttca aaaactgtct aaaagaaatt gactctacat tgtataagaa cttatttgtg 1860
gataagaata tgaagtatat tccaacagaa gatgtttcag gtctgtcact ggaagaacaa 1920
ttgaggaggt tgcaagaaga acgaacttgt aaagtgtgta tggacaaaga agtttctgtt 1980
gtatttattc cttgtggtca tctggtagta tgccaggaat gtgcccttc tctaagaaaa 2040
tgccctattt gcaggggtat aatcaagggt actgttcgta catttctctc ttaaagaaaa 2100
atagtctata ttttaacctg cataaaaagg tctttaaaat attgttgaac acttgaagcc 2160
atctaaaagta aaaagggaat tatgagtttt tcaattagta acattcatgt tctagtctgc 2220
tttggacta ataacttgtt ttctgaaaaag atggatatcat atatttaatc ttaatctgtt 2280
tatttacaag ggaagattta tgtttggtga actatattag tatgtatgtg tacctaaggg 2340
agtagcgtcn ctgcttgta tgcattcatt caggagttac tggatttgtt gttctttcag 2400
aaagctttga anactaaatt atagtgtaga aaagaactgg aaaccaggaa ctctggagtt 2460
catcagagtt atggtgccga attgtctttg gtgcttttca cttgtgtttt aaaataagga 2520
tttttctctt atttctcccc ctagtttgtg agaaacatct caataaagtg ctttaaaaaag 2580

```

<210> 8
 <211> 618
 <212> PRT
 <213> Homo sapiens

```

<400> 8
Met His Lys Thr Ala Ser Gln Arg Leu Phe Pro Gly Pro Ser Tyr Gln
  1             5             10             15
Asn Ile Lys Ser Ile Met Glu Asp Ser Thr Ile Leu Ser Asp Trp Thr
      20             25             30
Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr
      35             40             45
Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro Val Ser Glu
      50             55             60
Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val Asn Asp Lys
      65             70             75             80
Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp Lys Leu Gly
      85             90             95
Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser Cys Ser Phe
      100            105            110

```


Ile	Gln	Asn	Leu	Val	Ser	Ala	Ser	Leu	Gly	Ser	Thr	Ser	Lys	Asn	Thr
		115					120					125			
Ser	Pro	Met	Arg	Asn	Ser	Phe	Ala	His	Ser	Leu	Ser	Pro	Thr	Leu	Glu
		130				135					140				
His	Ser	Ser	Leu	Phe	Ser	Gly	Ser	Tyr	Ser	Ser	Leu	Pro	Pro	Asn	Pro
145					150					155					160
Leu	Asn	Ser	Arg	Ala	Val	Glu	Asp	Ile	Ser	Ser	Ser	Arg	Thr	Asn	Pro
				165					170					175	
Tyr	Ser	Tyr	Ala	Met	Ser	Thr	Glu	Glu	Ala	Arg	Phe	Leu	Thr	Tyr	His
			180					185					190		
Met	Trp	Pro	Leu	Thr	Phe	Leu	Ser	Pro	Ser	Glu	Leu	Ala	Arg	Ala	Gly
		195					200					205			
Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys	Gly
		210				215					220				
Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asp	Ala	Met	Ser	Glu	His
225					230					235					240
Arg	Arg	His	Phe	Pro	Asn	Cys	Pro	Phe	Leu	Glu	Asn	Ser	Leu	Glu	Thr
				245					250					255	
Leu	Arg	Phe	Ser	Ile	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala	Ala	Arg
			260					265					270		
Met	Arg	Thr	Phe	Met	Tyr	Trp	Pro	Ser	Ser	Val	Pro	Val	Gln	Pro	Glu
		275					280					285			
Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Arg	Asn	Asp	Asp	Val
		290				295					300				
Lys	Cys	Phe	Gly	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser	Gly	Asp
305					310					315					320
Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu	Phe	Leu
				325					330					335	
Ile	Arg	Met	Lys	Gly	Gln	Glu	Phe	Val	Asp	Glu	Ile	Gln	Gly	Arg	Tyr
			340				345						350		
Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Thr	Thr	Gly	Glu
		355					360					365			
Glu	Asn	Ala	Asp	Pro	Pro	Ile	Ile	His	Phe	Gly	Pro	Gly	Glu	Ser	Ser
		370				375					380				
Ser	Glu	Asp	Ala	Val	Met	Asn	Thr	Pro	Val	Val	Lys	Ser	Ala	Leu	
385					390				395						400
Glu	Met	Gly	Phe	Asn	Arg	Asp	Leu	Val	Lys	Gln	Thr	Val	Leu	Ser	Lys
				405					410					415	
Ile	Leu	Thr	Thr	Gly	Glu	Asn	Tyr	Lys	Thr	Val	Asn	Asp	Ile	Val	Ser
			420					425					430		
Ala	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Lys	Arg	Glu	Glu	Glu	Lys	Glu	Lys
		435					440					445			
Gln	Ala	Glu	Glu	Met	Ala	Ser	Asp	Asp	Leu	Ser	Leu	Ile	Arg	Lys	Asn
		450				455					460				
Arg	Met	Ala	Leu												

Met	Lys	Tyr	Ile	Pro	Thr	Glu	Asp	Val	Ser	Gly	Leu	Ser	Leu	Glu	Glu
545					550					555				560	
Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Met	Asp
				565					570					575	
Lys	Glu	Val	Ser	Val	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val	Cys
			580					585					590		
Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys	Arg	Gly	Ile
		595					600						605		
Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser						
	610						615								

<210> 9
 <211> 2100
 <212> DNA
 <213> Mus musculus

<400> 9

gacactctgc	tgggcggcgg	gccgccctcc	tccgggacct	cccctcggga	accgtcgccc	60
gcggcgctta	gttaggactg	gagtgccttg	cgcgaaaagg	tggacaagtc	ctattttcca	120
gagaagatga	cttttaacag	ttttgaagga	actagaactt	ttgtacttgc	agacaccaat	180
aaggatgaag	aattttaga	agagttaaat	agattaaaaa	catttgctaa	cttcccaagt	240
agtagcctg	tttcagcatc	aacattggcg	cgagctgggt	ttctttatac	cgggtgaagga	300
gacaccgtgc	aatgtttcag	ttgtcatgcg	gcaatagata	gatggcagta	tggagactca	360
gctgttgga	gacacaggag	aatatcccca	aattgcagat	ttatcaatgg	tttttatttt	420
gaaaaatgg	ctgcacagtc	tacaaatcct	ggtatccaaa	atggccagta	caaactctgaa	480
aactgtgtgg	gaaatagaaa	tccttttgcc	cctgacaggc	cacctgagac	tcatgctgat	540
tatctcttga	gaactggaca	ggtttagat	atttcagaca	ccatataccc	gaggaaccct	600
gccatgtgta	gtgaagaagc	cagattgaag	tcatttcaga	actggccgga	ctatgctcat	660
ttaaccccc	gagagttagc	tagtgctggc	ctctactaca	caggggctga	tgatcaagtg	720
caatgctttt	gttgtggggg	aaaactgaaa	aattgggaac	cctgtgatcg	tgcttggtca	780
gaacacagga	gacactttcc	caattgcttt	tttgttttgg	gccggaacgt	taatgttcga	840
agtgaatctg	gtgtgagttc	tgataggaat	ttcccaaatt	caacaaactc	tccaagaaat	900
ccagccatgg	cagaatatga	agcacggatc	gttacttttg	gaacatggat	atactcagtt	960
aacaaggagc	agcttgcaag	agctggattt	tatgctttag	gtgaaggcga	taaagtgaag	1020
tgcttccact	gtggaggagg	gctcacggat	tggaaagccaa	gtgaagaccc	ctgggaccag	1080
catgctaagt	gtacccagg	gtgcaaatat	ctattggatg	agaaggggca	agaatatata	1140
aataaatattc	atttaaccca	tccacttgag	gaatctttgg	gaagaactgc	tgaaaaaaca	1200
ccaccgctaa	ctaaaaaaat	cgatgatacc	atcttccaga	atcctatggg	gcaagaagct	1260
atacgaatgg	gatttagctt	caaggacctt	aagaaaacaa	tggaagaaaa	aatccaaaca	1320
tccgggagca	gctatctatc	acttgaggtc	ctgattgcag	atcttgtgag	tgctcagaaa	1380
gataatacgg	aggatgagtc	aagtcaaaact	tcattgcaga	aagacattag	tactgaagag	1440
cagctaaggc	gcctacaaga	ggagaagctt	tccaaaatct	gtatggatag	aaatattgct	1500
atcgtttttt	ttccttgtgg	acatctggcc	acttgtaaac	agtgtgcaga	agcagttgac	1560
aaatgtccca	tgtgctacac	cgtcattacg	ttcaaccaaa	aaatttttat	gtcttagtgg	1620
ggcaccacat	gttatgttct	tcttgctcta	attgaatgtg	taatgggagc	gaactttaag	1680
taatcctgca	tttgcatctc	attagcatcc	tgctgtttcc	aaatggagac	caatgctaac	1740
agcactgttt	ccgtctaaac	attcaatttc	tggatctttc	gagttatcag	ctgtatcatt	1800
tagccagtgt	tttactcgat	tgaaacctta	gacagagaag	catttttatag	cttttcacat	1860
gtatatgtgt	agtaactga	cttgatttct	atatgtaagt	gaattcatca	cctgcatggt	1920
tcatgccttt	tgcataagct	taacaaaatgg	agtgttctgt	ataagcatgg	agatgtgatg	1980
gaatctgccc	aatgacttta	attggcttat	tgtaaacacg	gaaagaactg	ccccacgctg	2040
ctgggaggat	aaagattggt	ttagatgctc	acttctgtgt	tttaggattc	tgccatttta	2100

004060" E424560

Phe	Lys	Asp	Leu	Lys	Lys	Thr	Met	Glu	Glu	Lys	Ile	Gln	Thr	Ser	Gly
385					390					395					400
Ser	Ser	Tyr	Leu	Ser	Leu	Glu	Val	Leu	Ile	Ala	Asp	Leu	Val	Ser	Ala
			405					410						415	
Gln	Lys	Asp	Asn	Thr	Glu	Asp	Glu	Ser	Ser	Gln	Thr	Ser	Leu	Gln	Lys
			420					425					430		
Asp	Ile	Ser	Thr	Glu	Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Lys	Leu
		435					440					445			
Ser	Lys	Ile	Cys	Met	Asp	Arg	Asn	Ile	Ala	Ile	Val	Phe	Phe	Pro	Cys
	450				455					460					
Gly	His	Leu	Ala	Thr	Cys	Lys	Gln	Cys	Ala	Glu	Ala	Val	Asp	Lys	Cys
465					470					475					480
Pro	Met	Cys	Tyr	Thr	Val	Ile	Thr	Phe	Asn	Gln	Lys	Ile	Phe	Met	Ser
			485					490						495	

<210> 11
 <211> 67
 <212> PRT
 <213> Orgyia pseudotsugata

<400> 11
 Lys Ala Ala Arg Leu Gly Thr Tyr Thr Asn Trp Pro Val Gln Phe Leu
 1 5 10 15
 Glu Pro Ser Arg Met Ala Ala Ser Gly Phe Tyr Tyr Leu Gly Arg Gly
 20 25 30
 Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Thr Asn Trp Val
 35 40 45
 Arg Gly Asp Asp Pro Glu Thr Asp His Lys Arg Trp Ala Pro Gln Cys
 50 55 60
 Pro Phe Val
 65

<210> 12
 <211> 275
 <212> PRT
 <213> Cydia pomonella

<400> 12
 Met Ser Asp Leu Arg Leu Glu Glu Val Arg Leu Asn Thr Phe Glu Lys
 1 5 10 15
 Trp Pro Val Ser Phe Leu Ser Pro Glu Thr Met Ala Lys Asn Gly Phe
 20 25 30
 Tyr Tyr Leu Gly Arg Ser Asp Glu Val Arg Cys Ala Phe Cys Lys Val
 35 40 45
 Glu Ile Met Arg Trp Lys Glu Gly Glu Asp Pro Ala Ala Asp His Lys
 50 55 60
 Lys Trp Ala Pro Gln Cys Pro Phe Val Lys Gly Ile Asp Val Cys Gly
 65 70 75 80
 Ser Ile Val Thr Thr Asn Asn Ile Gln Asn Thr Thr Thr His Asp Thr
 85 90 95
 Ile Ile Gly Pro Ala His Pro Lys Tyr Ala His Glu Ala Ala Arg Val
 100 105 110

001050"E44550

Lys	Ser	Phe	His	Asn	Trp	Pro	Arg	Cys	Met	Lys	Gln	Arg	Pro	Glu	Gln
		115					120					125			
Met	Ala	Asp	Ala	Gly	Phe	Phe	Tyr	Thr	Gly	Tyr	Gly	Asp	Asn	Thr	Lys
	130					135					140				
Cys	Phe	Tyr	Cys	Asp	Gly	Gly	Leu	Lys	Asp	Trp	Glu	Pro	Glu	Asp	Val
145					150					155					160
Pro	Trp	Glu	Gln	His	Val	Arg	Trp	Phe	Asp	Arg	Cys	Ala	Tyr	Val	Gln
				165					170					175	
Leu	Val	Lys	Gly	Arg	Asp	Tyr	Val	Gln	Lys	Val	Ile	Thr	Glu	Ala	Cys
			180					185					190		
Val	Leu	Pro	Gly	Glu	Asn	Thr	Thr	Val	Ser	Thr	Ala	Ala	Pro	Val	Ser
		195					200					205			
Glu	Pro	Ile	Pro	Glu	Thr	Lys	Ile	Glu	Lys	Glu	Pro	Gln	Val	Glu	Asp
	210					215					220				
Ser	Lys	Leu	Cys	Lys	Ile	Cys	Tyr	Val	Glu	Glu	Cys	Ile	Val	Cys	Phe
225					230					235					240
Val	Pro	Cys	Gly	His	Val	Val	Ala	Cys	Ala	Lys	Cys	Ala	Leu	Ser	Val
				245					250					255	
Asp	Lys	Cys	Pro	Met	Cys	Arg	Lys	Ile	Val	Thr	Ser	Val	Leu	Lys	Val
			260					265					270		
Tyr	Phe	Ser													
		275													

<210> 13
 <211> 498
 <212> PRT
 <213> Drosophila melanogaster

<400> 13

Met	Thr	Glu	Leu	Gly	Met	Glu	Leu	Glu	Ser	Val	Arg	Leu	Ala	Thr	Phe
1				5					10					15	
Gly	Glu	Trp	Pro	Leu	Asn	Ala	Pro	Val	Ser	Ala	Glu	Asp	Leu	Val	Ala
			20					25					30		
Asn	Gly	Phe	Phe	Ala	Thr	Gly	Lys	Trp	Leu	Glu	Ala	Glu	Cys	His	Phe
		35				40						45			
Cys	His	Val	Arg	Ile	Asp	Arg	Trp	Glu	Tyr	Gly	Asp	Gln	Val	Ala	Glu
	50					55					60				
Arg	His	Arg	Arg	Ser	Ser	Pro	Ile	Cys	Ser	Met	Val	Leu	Ala	Pro	Asn
65					70					75					80
His	Cys	Gly	Asn	Val	Pro	Arg	Ser	Gln	Glu	Ser	Asp	Asn	Glu	Gly	Asn
			85						90					95	
Ser	Val	Val	Asp	Ser	Pro	Glu	Ser	Cys	Ser	Cys	Pro	Asp	Leu	Leu	Leu
			100					105					110		
Glu	Ala	Asn	Arg	Leu	Val	Thr	Phe	Lys	Asp	Trp	Pro	Asn	Pro	Asn	Ile
		115					120					125			
Thr	Pro	Gln	Ala	Leu	Ala	Lys	Ala	Gly	Phe	Tyr	Tyr	Leu	Asn	Arg	Leu
	130					135					140				
Asp	His	Val	Lys	Cys	Val	Trp	Cys	Asn	Gly	Val	Ile	Ala	Lys	Trp	Glu
145					150					155					160
Lys	Asn	Asp	Asn	Ala	Phe	Glu	Glu	His	Lys	Arg	Phe	Phe	Pro	Gln	Cys
				165					170					175	
Pro	Arg	Val	Gln	Met	Gly	Pro	Leu	Ile	Glu	Phe	Ala	Thr	Gly	Lys	Asn
			180					185					190		

Leu	Asp	Glu	Leu	Gly	Ile	Gln	Pro	Thr	Thr	Leu	Pro	Leu	Arg	Pro	Lys
Tyr	Ala	Cys	Val	Asp	Ala	Arg	Leu	Arg	Thr	Phe	Thr	Asp	Trp	Pro	Ile
Ser	Asn	Ile	Gln	Pro	Ala	Ser	Ala	Leu	Ala	Gln	Ala	Gly	Leu	Tyr	Tyr
225					230					235					240
Gln	Lys	Ile	Gly	Asp	Gln	Val	Arg	Cys	Phe	His	Cys	Asn	Ile	Gly	Leu
Arg	Ser	Trp	Gln	Lys	Glu	Asp	Glu	Pro	Trp	Phe	Glu	His	Ala	Lys	Trp
Ser	Pro	Lys	Cys	Gln	Phe	Val	Leu	Leu	Ala	Lys	Gly	Pro	Ala	Tyr	Val
Ser	Glu	Val	Leu	Ala	Thr	Thr	Ala	Ala	Asn	Ala	Ser	Ser	Gln	Pro	Ala
Thr	Ala	Pro	Ala	Pro	Thr	Leu	Gln	Ala	Asp	Val	Leu	Met	Asp	Glu	Ala
305					310					315					320
Pro	Ala	Lys	Glu	Ala	Leu	Thr	Leu	Gly	Ile	Asp	Gly	Gly	Val	Val	Arg
Asn	Ala	Ile	Gln	Arg	Lys	Leu	Leu	Ser	Ser	Gly	Cys	Ala	Phe	Ser	Thr
Leu	Asp	Glu	Leu	Leu	His	Asp	Ile	Phe	Asp	Asp	Ala	Gly	Ala	Gly	Ala
Ala	Leu	Glu	Val	Arg	Glu	Pro	Pro	Glu	Pro	Ser	Ala	Pro	Phe	Ile	Glu
Pro	Cys	Gln	Ala	Thr	Thr	Ser	Lys	Ala	Ala	Ser	Val	Pro	Ile	Pro	Val
385					390					395					400
Ala	Asp	Ser	Ile	Pro	Ala	Lys	Pro	Gln	Ala	Ala	Glu	Ala	Val	Ser	Asn
Ile	Ser	Lys	Ile	Thr	Asp	Glu	Ile	Gln	Lys	Met	Ser	Val	Ser	Thr	Pro
Asn	Gly	Asn	Leu	Ser	Leu	Glu	Glu	Glu	Asn	Arg	Gln	Leu	Lys	Asp	Ala
Arg	Leu	Cys	Lys	Val	Cys	Leu	Asp	Glu	Glu	Val	Gly	Val	Val	Phe	Leu
Pro	Cys	Gly	His	Leu	Ala	Thr	Cys	Asn	Gln	Cys	Ala	Pro	Ser	Val	Ala
465					470					475					480
Asn	Cys	Pro	Met	Cys	Arg	Ala	Asp	Ile	Lys	Gly	Phe	Val	Arg	Thr	Phe
Leu	Ser				485					490					495

```
<210> 14
<211> 67
<212> PRT
<213> Cydia pomonella
```

<400> 14
Glu Glu Val Arg Leu Asn Thr Phe Glu Lys Trp Pro Val Ser Phe Leu
1 5 10 15
Ser Pro Glu Thr Met Ala Lys Asn Gly Phe Tyr Tyr Leu Gly Arg Ser
20 25 30
Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Met Arg Trp Lys
35 40 45

Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60
 Cys Phe Phe Val
 65

<210> 21
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 21
 Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
 1 5 10 15
 Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ile
 20 25 30
 Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
 35 40 45
 Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60
 Cys Phe Phe Val
 65

<210> 22
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 22
 Glu Asn Ala Arg Leu Leu Thr Phe Gln Thr Trp Pro Leu Thr Phe Leu
 1 5 10 15
 Ser Pro Thr Asp Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
 Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
 35 40 45
 Pro Lys Asp Asn Ala Met Ser Glu His Leu Arg His Phe Pro Lys Cys
 50 55 60
 Pro Phe Ile
 65

<210> 23
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 23
 Glu Glu Ala Arg Phe Leu Thr Tyr His Met Trp Pro Leu Thr Phe Leu
 1 5 10 15
 Ser Pro Ser Glu Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
 Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
 35 40 45

001000"EH45960

Pro Lys Asp Asp Ala Met Ser Glu His Arg Arg His Phe Pro Asn Cys
 50 55 60
 Pro Phe Leu
 65

<210> 24
 <211> 66
 <212> PRT
 <213> Mus musculus

<400> 24
 Tyr Glu Ala Arg Ile Val Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
 1 5 10 15
 Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
 20 25 30
 Lys Val Lys Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro
 35 40 45
 Ser Glu Asp Pro Trp Asp Gln His Ala Lys Cys Tyr Pro Gly Cys Lys
 50 55 60
 Tyr Leu
 65

<210> 25
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 25
 Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
 1 5 10 15
 Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
 20 25 30
 Lys Val Lys Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro
 35 40 45
 Ser Glu Asp Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys
 50 55 60
 Tyr Leu
 65

<210> 26
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 26
 His Ala Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu
 1 5 10 15
 Val Asn Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn
 20 25 30
 Ser Asp Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp
 35 40 45

00100100"090143"054743056500

Glu Ser Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg
 50 55 60
 Cys Glu Tyr Leu
 65

<210> 27
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 27
 His Ala Ala Arg Met Arg Thr Phe Met Tyr Trp Pro Ser Ser Val Pro
 1 5 10 15
 Val Gln Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Arg
 20 25 30
 Asn Asp Asp Val Lys Cys Phe Gly Cys Asp Gly Gly Leu Arg Cys Trp
 35 40 45
 Glu Ser Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg
 50 55 60
 Cys Glu Phe Leu
 65

<210> 28
 <211> 68
 <212> PRT
 <213> Orgyia pseudotsugata

<400> 28
 Glu Ala Ala Arg Leu Arg Thr Phe Ala Glu Trp Pro Arg Gly Leu Lys
 1 5 10 15
 Gln Arg Pro Glu Glu Leu Ala Glu Ala Gly Phe Phe Tyr Thr Gly Gln
 20 25 30
 Gly Asp Lys Thr Arg Cys Phe Cys Cys Asp Gly Gly Leu Lys Asp Trp
 35 40 45
 Glu Pro Asp Asp Ala Pro Trp Gln Gln His Ala Arg Trp Tyr Asp Arg
 50 55 60
 Cys Glu Tyr Val
 65

<210> 29
 <211> 68
 <212> PRT
 <213> Cydia pomonella

<400> 29
 Glu Ala Ala Arg Val Lys Ser Phe His Asn Trp Pro Arg Cys Met Lys
 1 5 10 15
 Gln Arg Pro Glu Gln Met Ala Asp Ala Gly Phe Phe Tyr Thr Gly Tyr
 20 25 30
 Gly Asp Asn Thr Lys Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp
 35 40 45

Glu Pro Glu Asp Val Pro Trp Glu Gln His Val Arg Trp Phe Asp Arg
 50 55 60
 Cys Ala Tyr Val
 65

<210> 30
 <211> 68
 <212> PRT
 <213> Drosophila melanogaster

<400> 30
 Val Asp Ala Arg Leu Arg Thr Phe Thr Asp Trp Pro Ile Ser Asn Ile
 1 5 10 15
 Gln Pro Ala Ser Ala Leu Ala Gln Ala Gly Leu Tyr Tyr Gln Lys Ile
 20 25 30
 Gly Asp Gln Val Arg Cys Phe His Cys Asn Ile Gly Leu Arg Ser Trp
 35 40 45
 Gln Lys Glu Asp Glu Pro Trp Phe Glu His Ala Lys Trp Ser Pro Lys
 50 55 60
 Cys Gln Phe Val
 65

<210> 31
 <211> 66
 <212> PRT
 <213> Drosophila melanogaster

<400> 31
 Glu Ser Val Arg Leu Ala Thr Phe Gly Glu Trp Pro Leu Asn Ala Pro
 1 5 10 15
 Val Ser Ala Glu Asp Leu Val Ala Asn Gly Phe Phe Gly Thr Trp Met
 20 25 30
 Glu Ala Glu Cys Asp Phe Cys His Val Arg Ile Asp Arg Trp Glu Tyr
 35 40 45
 Gly Asp Leu Val Ala Glu Arg His Arg Arg Ser Ser Pro Ile Cys Ser
 50 55 60
 Met Val
 65

<210> 32
 <211> 46
 <212> PRT
 <213> Homo sapiens

001050"CH45960

<400> 32

Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Met
1				5					10					15	
Asp	Lys	Glu	Val	Ser	Val	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val
		20						25					30		
Cys	Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys		
		35					40					45			

<210> 33

<211> 46

<212> PRT

<213> Homo sapiens

<400> 33

Glu	Gln	Leu	Arg	Arg	Leu	Pro	Glu	Glu	Arg	Thr	Cys	Lys	Val	Cys	Met
1				5					10					15	
Asp	Lys	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val
		20						25					30		
Cys	Lys	Asp	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys		
		35					40					45			

<210> 34

<211> 46

<212> PRT

<213> Homo sapiens

<400> 34

Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Lys	Leu	Ser	Lys	Ile	Cys	Met
1				5					10					15	
Asp	Arg	Asn	Ile	Ala	Ile	Val	Phe	Phe	Pro	Cys	Gly	His	Leu	Ala	Thr
		20						25					30		
Cys	Lys	Gln	Cys	Ala	Glu	Ala	Val	Asp	Lys	Cys	Pro	Met	Cys		
		35					40					45			

<210> 35

<211> 46

<212> PRT

<213> Homo sapiens

<400> 35

Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Lys	Leu	Cys	Lys	Ile	Cys	Met
1				5					10					15	
Asp	Arg	Asn	Ile	Ala	Ile	Val	Phe	Val	Pro	Cys	Gly	His	Leu	Val	Thr
		20						25					30		
Cys	Lys	Gln	Cys	Ala	Glu	Ala	Val	Asp	Lys	Cys	Pro	Met	Cys		
		35					40					45			

<210> 36
 <211> 46
 <212> PRT
 <213> *Drosophila melanogaster*

<400> 36
 Glu Glu Asn Arg Gln Leu Lys Asp Ala Arg Leu Cys Lys Val Cys Leu
 1 5 10 15
 Asp Glu Glu Val Gly Val Val Phe Leu Pro Cys Gly His Leu Ala Thr
 20 25 30
 Cys Asn Gln Cys Ala Pro Ser Val Ala Asn Cys Pro Met Cys
 35 40 45

<210> 37
 <211> 46
 <212> PRT
 <213> *Cydia pomonella*

<400> 37
 Glu Lys Glu Pro Gln Val Glu Asp Ser Lys Leu Cys Lys Ile Cys Tyr
 1 5 10 15
 Val Glu Glu Cys Ile Val Cys Phe Val Pro Cys Gly His Val Val Ala
 20 25 30
 Cys Ala Lys Cys Ala Leu Ser Val Asp Lys Cys Pro Met Cys
 35 40 45

<210> 38
 <211> 46
 <212> PRT
 <213> *Orgyia pseudotsugata*

<400> 38
 Ala Val Glu Ala Glu Val Ala Asp Asp Arg Leu Cys Lys Ile Cys Leu
 1 5 10 15
 Gly Ala Glu Lys Thr Val Cys Phe Val Pro Cys Gly His Val Val Ala
 20 25 30
 Cys Gly Lys Cys Ala Ala Gly Val Thr Thr Cys Pro Val Cys
 35 40 45

<210> 39
 <211> 2474
 <212> DNA
 <213> *Mus musculus*

<400> 39
 gaattccggg agacctacac ccccgagat cagaggatcat tgctggcggt cagagcctag 60
 gaagtgggct gcggtatcag cctagcagta aaaccgacca gaagccatgc acaaaactac 120
 atccccagag aaagacttgt cccttcccct ccctgtcatc tcaccatgaa catggttcaa 180
 gacagcgcct ttctagccaa gctgatgaag agtgctgaca cctttgagtt gaagtatgac 240
 ttttcctgtg agctgtaccg attgtccacg tattcagctt ttcccagggg agttcctgtg 300

001050" E445960

tcagaaagga	gtctggctcg	tgctggcttt	tactacactg	gtgccaatga	caaggtcaag	360
tgcttctgct	gtggcctgat	gctagacaac	tggaaacaag	gggacagtcc	catggagaag	420
cacagaaagt	tgtaccccag	ctgcaacttt	gtacagactt	tgaatccagc	caacagttctg	480
gaagctagtc	ctcggccttc	tcttccttcc	acggcgatga	gcaccatgcc	tttgagcttt	540
<u>gcaagttctg</u>	<u>agaatactgg</u>	<u>ctatttcagt</u>	<u>ggctcttact</u>	<u>cgagctttcc</u>	<u>ctcagaccct</u>	600
gtgaacttcc	gagcaaatca	agattgtcct	gctttgagca	caagtcccta	ccacttttgca	660
atgaacacag	agaaggccag	attactcacc	tatgaaacat	ggccattgtc	ttttctgtca	720
ccagcaaagc	tggccaaagc	aggcttctac	tacataggac	ctggagatag	agtggcctgc	780
tttgctgctg	atgggaaact	gagcaactgg	gaacgtaagg	atgatgctat	gtcagagcac	840
cagaggcatt	tcccagctg	tccgttctta	aaagacttgg	gtcagttctgc	ttcgagatac	900
actgtctcta	acctgagcat	gcagacacac	gcagcccgtg	ttagaacatt	ctctaactgg	960
ccttctagt	cactagttca	ttcccaggaa	cttgcaagt	cgggctttta	ttatacagga	1020
cacagtgatg	atgtcaagt	tttatgctgt	gatggtgggc	tgaggtgctg	ggaatctgga	1080
gatgaccct	gggtggaaca	tgccaagtgg	tttccaaggt	gtgagtactt	gtcagaatc	1140
aaaggccaag	aatttgtcag	ccaagttcaa	gctggctatc	ctcatctact	tgagcagcta	1200
ttatctacgt	cagactcccc	agaagatgag	aatgcagacg	cagcaactcg	gcattttggc	1260
cctggagaaa	gttcggaaga	tgctgctcat	atgacacgcg	ctgtggttaa	agcagccttg	1320
gaaatgggct	tcagtaggag	cttggtgatg	cagacggttc	agtggcagat	cctggccact	1380
ggtgagaact	acaggaccgt	cagtgacctc	gttataggct	tactcgatgc	agaagacgag	1440
atgagagagg	agcagatgga	gcaggcggcc	gaggaggagg	agtcagatga	tctagcacta	1500
atccggaaga	acaaaatggt	gctttttccaa	catttgacgt	gtgtgacacc	aatgctgtat	1560
tgctcctaa	gtgcaagggc	catcactgaa	caggagtgca	atgctgtgaa	acagaaacca	1620
cacaccttac	aagcaagcac	actgattgat	actgtgttag	caaaaggaaa	cactgcagca	1680
acctcattca	gaaactccct	tcgggaaatt	gacctgcgt	tatacagaga	tatatattgtg	1740
caacaggaca	ttaggagttc	tcccacagat	gacattgcag	ctctaccaat	ggaagaacag	1800
ttgcggcccc	tcccgaggga	cagaatgtgt	aaagtgtgta	tggaccgaga	ggtatccatc	1860
gtgttcattc	cctgtggcca	tctggctcgtg	tgcaaagact	gcgtcccttc	tctgaggaag	1920
tgtcccattc	gtagagggac	catcaagggc	acagtgcgca	cattttctctc	ctgaacaaga	1980
ctaattggtc	atggctgcaa	cttcagccag	gaggaagttc	actgtcactc	ccagttccat	2040
tcggaacttg	aggccagcct	ggatagcacg	agacaccgcc	aaacacacaa	atataaacat	2100
gaaaaacttt	tgtctgaagt	caagaatgaa	tgaattactt	atataataat	tttaattggt	2160
ttccttaaaa	gtgctatttg	ttcccaactc	agaaaattgt	tttctgtaaa	catatttaca	2220
tactacctgc	atctaaagta	ttcatattat	catatattca	gatgtcatga	gagagggttt	2280
tgttcttggt	cctgaaaagc	tggtttatca	tctgatcagc	ataactgcg	caacgggcag	2340
ggctagaatc	catgaaccaa	gctgcaaaga	tctcacgcta	aataaggcgg	aaagatttgg	2400
agaaagcaa	ggaaattctt	tccgtgtccaa	tgtatactct	tcagactaat	gacctcttcc	2460
tatcaagcct	tcta					2474

```
<210> 40
<211> 602
<212> PRT
<213> Mus musculus
```

<400> 40															
Met	Asn	Met	Val	Gln	Asp	Ser	Ala	Phe	Leu	Ala	Lys	Leu	Met	Lys	Ser
1				5					10					15	
Ala	Asp	Thr	Phe	Glu	Leu	Lys	Tyr	Asp	Phe	Ser	Cys	Glu	Leu	Tyr	Arg
			20					25					30		
Leu	Ser	Thr	Tyr	Ser	Ala	Phe	Pro	Arg	Gly	Val	Pro	Val	Ser	Glu	Arg
		35					40					45			
Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Ala	Asn	Asp	Lys	Val
	50					55					60				
Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Gln	Gly	Asp
65					70				75						80

Ser	Pro	Met	Glu	Lys	His	Arg	Lys	Leu	Tyr	Pro	Ser	Cys	Asn	Phe	Val
Gln	Thr	Leu	Asn	Pro	Ala	Asn	Ser	Leu	Glu	Ala	Ser	Pro	Arg	Pro	Ser
Leu	Pro	Ser	Thr	Ala	Met	Ser	Thr	Met	Pro	Leu	Ser	Phe	Ala	Ser	Ser
			115				120					125			
Glu	Asn	Thr	Gly	Tyr	Phe	Ser	Gly	Ser	Tyr	Ser	Ser	Phe	Pro	Ser	Asp
			130				135					140			
Pro	Val	Asn	Phe	Arg	Ala	Asn	Gln	Asp	Cys	Pro	Ala	Leu	Ser	Thr	Ser
145					150					155					160
Pro	Tyr	His	Phe	Ala	Met	Asn	Thr	Glu	Lys	Ala	Arg	Leu	Leu	Thr	Tyr
				165					170					175	
Glu	Thr	Trp	Pro	Leu	Ser	Phe	Leu	Ser	Pro	Ala	Lys	Leu	Ala	Lys	Ala
			180					185				190			
Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys
			195				200					205			
Asp	Gly	Lys	Leu	Ser	Asn	Trp	Glu	Arg	Lys	Asp	Asp	Ala	Met	Ser	Glu
			210			215					220				
His	Gln	Arg	His	Phe	Pro	Ser	Cys	Pro	Phe	Leu	Lys	Asp	Leu	Gly	Gln
225					230					235					240
Ser	Ala	Ser	Arg	Tyr	Thr	Val	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala
				245					250					255	
Ala	Arg	Ile	Arg	Thr	Phe	Ser	Asn	Trp	Pro	Ser	Ser	Ala	Leu	Val	His
			260					265					270		
Ser	Gln	Glu	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	His	Ser	Asp
			275				280					285			
Asp	Val	Lys	Cys	Leu	Cys	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser
			290			295					300				
Gly	Asp	Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu
305				310					315						320
Tyr	Leu	Leu	Arg	Ile	Lys	Gly	Gln	Glu	Phe	Val	Ser	Gln	Val	Gln	Ala
				325					330					335	
Gly	Tyr	Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Ser	Pro
			340					345					350		
Glu	Asp	Glu	Asn	Ala	Asp	Ala	Ala	Ile	Val	His	Phe	Gly	Pro	Gly	Glu
			355				360					365			
Ser	Ser	Glu	Asp	Val	Val	Met	Met	Ser	Thr	Pro	Val	Val	Lys	Ala	Ala
			370			375					380				
Leu	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Arg	Gln	Thr	Val	Gln	Trp
385				390						395					400
Gln	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Thr	Val	Ser	Asp	Leu	Val
				405					410					415	
Ile	Gly	Leu	Leu	Asp	Ala	Glu	Asp	Glu	Met	Arg	Glu	Glu	Gln	Met	Glu
			420					425					430		
Gln	Ala	Ala	Glu	Glu	Glu	Glu	Ser	Asp	Asp	Leu	Ala	Leu	Ile	Arg	Lys
			435				440					445			

Arg	Glu	Ile	Asp	Pro	Ala	Leu	Tyr	Arg	Asp	Ile	Phe	Val	Gln	Gln	Asp
515				520				525							
Ile	Arg	Ser	Leu	Pro	Thr	Asp	Asp	Ile	Ala	Ala	Leu	Pro	Met	Glu	Glu
530				535				540							
Gln	Leu	Arg	Pro	Leu	Pro	Glu	Asp	Arg	Met	Cys	Lys	Val	Cys	Met	Asp
545				550				555				560			
Arg	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly	His	Leu	Val	Val	Cys
565				570				575							
Lys	Asp	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro	Ile	Cys	Arg	Gly	Thr
580				585				590							
Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser						
595				600											

<210> 41
 <211> 2416
 <212> DNA
 <213> Mus musculus

<400> 41
 ctgtggtgga gatctattgt ccaagtgggtg agaaacttca tctggaagtt taagcgggtca 60
 gaaatactat tactactcat ggacaaaact gtctcccaga gactcgccca aggtacctta 120
 cacccaaaaa cttaaactgta taatggagaa gagcacaatc ttgtcaaatt ggacaaagga 180
 gagcgaagaa aaaatgaagt ttgacttttc gtgtgaactc taccgaatgt ctacatattc 240
 agcttttccc aggggagttc ctgtctcaga gaggagtctg gctcgtgctg gcttttatta 300
 tacagggtgtg aatgacaaaag tcaagtgcct ctgctgtggc ctgatgttgg ataactggaa 360
 acaaggggac agtcctgttg aaaagcacag acagttctat cccagctgca gctttgtaca 420
 gactctgctt tcagccagtc tgcagtcctc atctaagaat atgtctcctg tgaaaagtag 480
 atttgacat tcgtcacctc tggaaacgagg tggcattcac tccaacctgt gctctagccc 540
 tcttaattct agagcagtg aagacttctc atcaaggatg gatccctgca gctatgccat 600
 gagtacagaa gaggccagat ttcttactta cagtatgtgg cctttaagtt ttctgtcacc 660
 agcagagctg gccagagctg gcttctatta catagggcct ggagacaggg tggcctgttt 720
 tgctgtggt gggaaactga gcaactggga accaaaggat tatgctatgt cagagcaccg 780
 cagacatttt cccactgtc catttctgga aaatacttca gaaacacaga ggtttagtat 840
 atcaaatcta agtatgcaga cacactctgc tcgattgagg acatttctgt actggccacc 900
 tagtgttctt gttcagcccg agcagcttgc aagtgtgga ttctattacg tggatcgcaa 960
 tgaatgatgtc aagtgccttt gttgtgatgg tggcttgaga tgttggaac ctggagatga 1020
 cccctggata gaacacgcca aatggtttcc aagggtgtgag ttcttgatac ggatgaaggg 1080
 tcaggagttt gttgatgaga ttcaagctag atatcctcat cttcttgagc agctgttgtc 1140
 cacttcagac accccaggag aagaaaatgc tgaccctaca gagacagtgg tgcatttttg 1200
 ccctggagaa agttcgaaag atgtcgtcat gatgagcacg cctgtggtta aagcagcctt 1260
 ggaaatgggc ttcagtagga gcctggtgag acagacggtt cagcggcaga tcctggccac 1320
 tggtgagaac tacaggaccg tcaatgatat tgtctcagta cttttgaatg ctgaagatga 1380
 gagaagagaa gaggagaagg aaagacagac tgaagagatg gcatcaggtg acttatcact 1440
 gattcggaaag aatagaatgg ccctctttca acagttgaca catgtccttc ctatcctgga 1500
 taatcttctt gaggccagtg taattacaaa acaggaacat gatattatta gacagaaaac 1560
 acagataccc ttacaagcaa gagagcttat tgacaccgtt ttagtcaagg gaaatgctgc 1620
 agccaacatc ttcaaaaact ctctgaaggg aattgactcc acgttatatg aaaacttatt 1680
 tgtggaaaag aatatgaagt atattccaac agaagacgtt tcaggcttgt cattggaaga 1740
 gcagttgcgg agattacaag aagaacgaac ttgcaaagtg tgtatggaca gagaggtttc 1800
 tattgtgttc attccgtgtg gtcacttagt agtctgccag gaatgtgccc cttctctaag 1860
 gaagtgtccc atctgcaggg ggacaatcaa ggggactgtg cgcacatttc tctcatgagt 1920
 gaagaatggt ctgaaagtat tgttggacat cagaagctgt cagaacaag aatgaactac 1980
 tgatttcagc tcttcagcag gacattctac tctctttcaa gattagtaat cttgctttat 2040

001060" E4743 0954743

Gln	Ala	Arg	Tyr	Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp
				325					330					335	
Thr	Pro	Gly	Glu	Glu	Asn	Ala	Asp	Pro	Thr	Glu	Thr	Val	Val	His	Phe
			340					345					350		
Gly	Pro	Gly	Glu	Ser	Ser	Lys	Asp	Val	Val	Met	Met	Ser	Thr	Pro	Val
			355					360					365		
Val	Lys	Ala	Ala	Leu	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Arg	Gln
			370					375					380		
Thr	Val	Gln	Arg	Gln	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Thr	Val
					390					395					400
Asn	Asp	Ile	Val	Ser	Val	Leu	Leu	Asn	Ala	Glu	Asp	Glu	Arg	Arg	Glu
				405					410					415	
Glu	Glu	Lys	Glu	Arg	Gln	Thr	Glu	Glu	Met	Ala	Ser	Gly	Asp	Leu	Ser
			420					425					430		
Leu	Ile	Arg	Lys	Asn	Arg	Met	Ala	Leu	Phe	Gln	Gln	Leu	Thr	His	Val
			435					440					445		
Leu	Pro	Ile	Leu	Asp	Asn	Leu	Leu	Glu	Ala	Ser	Val	Ile	Thr	Lys	Gln
			450					455					460		
Glu	His	Asp	Ile	Ile	Arg	Gln	Lys	Thr	Gln	Ile	Pro	Leu	Gln	Ala	Arg
					470					475					480
Glu	Leu	Ile	Asp	Thr	Val	Leu	Val	Lys	Gly	Asn	Ala	Ala	Ala	Asn	Ile
				485					490					495	
Phe	Lys	Asn	Ser	Leu	Lys	Gly	Ile	Asp	Ser	Thr	Leu	Tyr	Glu	Asn	Leu
			500					505					510		
Phe	Val	Glu	Lys	Asn	Met	Lys	Tyr	Ile	Pro	Thr	Glu	Asp	Val	Ser	Gly
			515					520					525		
Leu	Ser	Leu	Glu	Glu	Gln	Leu	Arg	Arg	Leu	Gln	Glu	Glu	Arg	Thr	Cys
			530					535					540		
Lys	Val	Cys	Met	Asp	Arg	Glu	Val	Ser	Ile	Val	Phe	Ile	Pro	Cys	Gly
					550					555					560
His	Leu	Val	Val	Cys	Gln	Glu	Cys	Ala	Pro	Ser	Leu	Arg	Lys	Cys	Pro
				565					570					575	
Ile	Cys	Arg	Gly	Thr	Ile	Lys	Gly	Thr	Val	Arg	Thr	Phe	Leu	Ser	
			580					585					590		

<210> 43
 <211> 11
 <212> PRT
 <213> artificial sequence based on Homo sapiens

<400> 43
 Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 1 5 10

<210> 44
 <211> 635
 <212> PRT
 <213> artificial sequence based on Homo sapiens, Mus musculus, Cydia pomonella, and Drosophila melanogaster

THE UNIVERSITY OF CHICAGO

<400> 44

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5				10					15		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa	Glu	Xaa	Xaa	Arg
			20					25				30			
Leu	Xaa	Thr	Phe	Xaa	Xaa	Phe	Pro	Xaa	Xaa	Xaa	Pro	Val	Ser	Xaa	Xaa
		35					40					45			
Xaa	Leu	Ala	Arg	Ala	Gly	Phe	Xaa	Tyr	Thr	Gly	Xaa	Xaa	Asp	Xaa	Val
	50					55					60				
Xaa	Cys	Phe	Xaa	Cys	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Trp	Xaa	Xaa	Gly	Asp
65				70						75				80	
Ser	Xaa	Xaa	Xaa	Xaa	His	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Cys	Xaa	Phe	Ile
				85					90					95	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			100					105					110		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Xaa	Xaa	Xaa
			115					120				125			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa
	130					135					140				
Xaa	Xaa	Xaa	Xaa	Xaa	Arg	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145				150					155						160
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Asp	Xaa	Ser	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				165					170					175	
Xaa	Xaa	Xaa	Met	Xaa	Xaa	Glu	Glu	Ala	Arg	Leu	Xaa	Thr	Phe	Xaa	Xaa
			180					185					190		
Trp	Pro	Xaa	Xaa	Xaa	Xaa	Leu	Xaa	Pro	Xaa	Glu	Leu	Ala	Xaa	Ala	Gly
		195					200					205			
Phe	Tyr	Tyr	Xaa	Gly	Xaa	Xaa	Asp	Xaa	Val	Xaa	Cys	Phe	Xaa	Cys	Gly
	210					215					220				
Gly	Lys	Leu	Xaa	Asn	Trp	Glu	Pro	Xaa	Asp	Xaa	Ala	Xaa	Ser	Glu	His
225				230						235				240	
Xaa	Arg	His	Phe	Pro	Xaa	Cys	Pro	Phe	Val	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
				245					250					255	
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Xaa	Xaa
			260					265					270		
Ser	Xaa	Xaa	Xaa	Pro	Xaa	Asn	Pro	Xaa	Met	Ala	Xaa	Xaa	Xaa	Ala	Arg
		275					280					285			
Xaa	Xaa	Thr	Phe	Xaa	Xaa	Trp	Pro	Xaa	Ser	Xaa	Xaa	Val	Xaa	Xaa	Glu
	290					295					300				
Gln	Leu	Ala	Xaa	Ala	Gly	Phe	Tyr	Tyr	Xaa	Gly	Xaa	Gly	Asp	Xaa	Val
305				310						315				320	
Lys	Cys	Phe	Xaa	Cys	Xaa	Gly	Gly	Leu	Xaa	Xaa	Trp	Xaa	Xaa	Xaa	Asp
				325					330					335	
Asp	Pro	Trp	Xaa	Gln	His	Ala	Lys	Trp	Phe	Pro	Xaa	Cys	Xaa	Tyr	Leu
			340					345					350		

007060"12445960

Xaa	Xaa	Xaa	Lys	Gly	Gln	Glu	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
355						360						365					
Xaa	Xaa	Leu	Xaa	Glu	Xaa	Leu	Xaa	Xaa	Thr	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
370						375						380					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	
385						390						395			400		
Xaa	Xaa	Asp	Xaa	Val	Xaa	Xaa	Xaa	Xaa	Pro	Xaa	Val	Xaa	Xaa	Ala	Xaa	Xaa	
			405						410						415		
Xaa	Met	Gly	Phe	Xaa	Xaa	Xaa	Xaa	Val	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Xaa	
			420						425						430		
Ile	Xaa	Xaa	Xaa	Gly	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Xaa	Xaa	Leu	Val	Xaa	Xaa	
435						440						445					
Asp	Leu	Xaa	Xaa	Ala	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Glu	Xaa	Xaa	Xaa	Xaa	
450						455						460					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
465						470						475			480		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
			485						490						495		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
			500						505						510		
Xaa	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	Leu	Gln	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
515						520						525					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
530						535						540					
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	
545						550						555			560		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Ser	Xaa	Glu	Glu	Xaa	
			565						570						575		
Gln	Leu	Arg	Arg	Leu	Xaa	Glu	Glu	Xaa	Leu	Cys	Lys	Xaa	Cys	Met	Asp	Xaa	
			580						585						590		
Xaa	Glu	Val	Xaa	Xaa	Val	Phe	Xaa	Pro	Cys	Gly	His	Leu	Val	Xaa	Cys	Xaa	
595						600						605					
Xaa	Xaa	Cys	Ala	Xaa	Ser	Val	Xaa	Lys	Cys	Pro	Met	Cys	Arg	Xaa	Xaa	Xaa	
610						615						620					
Ile	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Phe	Leu	Ser	Xaa							
625			630						635								

<210> 45
 <211> 204
 <212> DNA
 <213> Homo sapiens

<400> 45
 gagttttaata gattaaaaac ttttgctaata tttccaagtg gtagtcctgt ttcagcatca 60
 aacttggtcac gagcagggtt tctttataact ggtgaaggag ataccgtgcg gtgcttttagt 120
 tgtcatgcag ctgtagatag atggcaatat ggagactcag cagttggaag acacaggaaa 180
 gtatccccaa attgcagatt tatc 204

<210> 46
 <211> 204
 <212> DNA
 <213> Homo sapiens

<400> 51
 tatgaagcac ggatcggttac ttttgggaaca tggatataact cagttaacaa ggagcagctt 60
 gcaagagctg gatttttatgc ttttaggtgaa ggcgataaag tgaagtgtctt ccactgtgga 120
 ggagggtctca cggattggaa gccaaagtga gacccctggg accagcatgc taagtgtctac 180
 ccagggtgca aataccta 198

<210> 52
 <211> 138
 <212> DNA
 <213> Mus musculus

<400> 52
 gagcagctaa ggcgcctaca agaggagaag ctttccaaaa tctgtatgga tagaaatatt 60
 gctatcggtt tttttccttg tggacatctg gccacttgta aacagtgtgc agaagcagtt 120
 gacaaatgtc ccatgtgc 138

<210> 53
 <211> 204
 <212> DNA
 <213> Homo sapiens

<400> 53
 gaactgtacc gaatgtctac gtattccact tttcctgctg gggttcctgt ctcagaaaagg 60
 agtcttgctc gtgctgggtt ctattacact ggtgtgaatg acaagggtcaa atgcttctgt 120
 tgtggcctga tgctggataa ctggaaaaga ggagacagtc ctactgaaaa gcataaaaaag 180
 ttgtatccta gctgcagatt cggt 204

<210> 54
 <211> 201
 <212> DNA
 <213> Homo sapiens

<400> 54
 gaaaaatgcc gattacttac ttttcagaca tggccattga cttttctgtc gccaacagat 60
 ctggcacgag caggctttta ctacatagga cctggagaca gagtgggttg ctttgctgt 120
 ggtggaaaat tgagcaattg ggaaccgaag gataatgcta tgtcagaaca cctgagacat 180
 tttcccaaat gccatttat a 201

<210> 55
 <211> 204
 <212> DNA
 <213> Homo sapiens

<400> 55
 catgcagccc gcttttaaac attctttaac tggccctcta gtgttctagt taatcctgag 60
 cagcttgcaa gtgcgggttt ttattatgtg ggtaacagtg atgatgtcaa atgcttttgc 120
 tgtgatgggtg gactcaggtg ttgggaatct ggagatgatc catgggttca acatgccaaag 180
 tggtttccaa ggtgtgagta cttg 204

<210> 56
 <211> 138
 <212> DNA
 <213> Homo sapiens

<400> 56
gaacaattgc ggagactacc agaagaaaga acatgtaaag tgtgtatgga caaagaagtg 60
tccatagtgt ttattccttg tggcatccta gtagtatgca aagattgtgc tccttcttta 120
agaaagtgtc ctatttgt 138

<210> 57
<211> 203
<212> DNA
<213> Mus musculus

<400> 57
agctgtaccg attgtccacg tattcagctt ttcccagggg agttcctgtg tcagaaagga 60
gtctggctcg tgctggcttt tactacactg gtgccaatga caaggtcaag tgcttctgct 120
gtggcctgat gctagacaac tggaaacaag gggacagtcc catggagaag cacagaaagt 180
tgtacccag ctgcaacttt gta 203

<210> 58
<211> 201
<212> DNA
<213> Mus musculus

<400> 58
gagaaggcca gattactcac ctatgaaaca tggccattgt cttttctgtc accagcaaag 60
ctggccaaag caggcttcta ctacatagga cctggagata gagggtcctg ctttgcgtgc 120
gatgggaaac tgagcaactg ggaacgtaag gatgatgcta tgtcagagca ccagaggcat 180
ttcccagct gtccgttctt a 201

<210> 59
<211> 204
<212> DNA
<213> Mus musculus

<400> 59
cacgcagccc gtattagaac attctctaac tggccttcta gtgcactagt tcattcccag 60
gaacttgcaa gtgcgggctt ttattataca ggacacagtg atgatgtcaa gtgtttatgc 120
tgtgatgggtg ggctgagggtg ctgggaatct ggagatgacc cctgggtgga acatgccaa 180
tggtttccaa ggtgtgagta cttg 204

<210> 60
<211> 138
<212> DNA
<213> Mus musculus

<400> 60
gaacagtgtc ggcccctccc ggaggacaga atgtgtaaag tgtgtatgga ccgagaggta 60
tccatcgtgt tcattccctg tggccatctg gtcgtgtgca aagactgcgc tccctctctg 120
aggaagtgtc ccatctgt 138

<210> 61
<211> 204
<212> DNA
<213> Homo sapiens

<400> 66
gaagaggcca gatttcttac ttacagtatg tggcctttaa gttttctgtc accagcagag 60
ctggccagag ctggcttcta ttacataggg cctggagaca gggaggcctg ttttgcctgt 120
ggtaggaaac tgagcaactg ggaaccaaag gattatgcta tgcagagca ccgcagacat 180
ttccccact gtccatttct g 201

<210> 67
<211> 204
<212> DNA
<213> Mus musculus

<400> 67
cactctgctc gattgaggac atttctgtac tggccaccta gtgttcctgt tcagcccag 60
cagcttgcaa gtgctggatt ctattacgtg gatcgcaatg atgatgtcaa gtgcctttgt 120
tgtgatgggtg gcttgagatg ttgggaacct ggagatgacc cctggataga acacgccaaa 180
tggtttccaa ggtgtgagtt cttg 204

<210> 68
<211> 114
<212> DNA
<213> Mus musculus

<400> 68
gaacgaactt gcaaagtgtg tatggacaga gaggtttcta ttgtgttcat tccgtgtggt 60
catctagtag tctgccagga atgtgcccct tctctaagga agtgcccat ctgc 114

<210> 69
<211> 68
<212> PRT
<213> Homo sapiens

<400> 69
Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Gly Ser Pro
1 5 10 15
Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
20 25 30
Gly Asp Thr Val Arg Cys Phe Ser Cys His Ala Ala Val Asp Arg Trp
35 40 45
Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Lys Val Ser Pro Asn
50 55 60
Cys Arg Phe Ile
65

<210> 70
<211> 68
<212> PRT
<213> Homo sapiens

<400> 70
Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
1 5 10 15
Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ile
20 25 30

Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
 35 40 45
 Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60
 Cys Phe Phe Val
 65

<210> 71
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 71
 Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
 1 5 10 15
 Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
 20 25 30
 Lys Val Lys Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro
 35 40 45
 Ser Glu Asp Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys
 50 55 60
 Tyr Leu
 65

<210> 72
 <211> 46
 <212> PRT
 213> Homo sapiens

<400> 72
 Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Cys Lys Ile Cys Met
 1 5 10 15
 Asp Arg Asn Ile Ala Ile Val Phe Val Pro Cys Gly His Leu Val Thr
 20 25 30
 Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
 35 40 45

<210> 73
 <211> 68
 <212> PRT
 <213> Mus musculus

<400> 73
 Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Ser Ser Pro
 1 5 10 15
 Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
 20 25 30
 Gly Asp Thr Val Gln Cys Phe Ser Cys His Ala Ala Ile Asp Arg Trp
 35 40 45

Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Arg Ile Ser Pro Asn
 50 55 60
 Cys Arg Phe Ile
 65

<210> 74
 <211> 68
 <212> PRT
 <213> Mus musculus

<400> 74
 Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
 1 5 10 15
 Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ala
 20 25 30
 Asp Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
 35 40 45
 Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60
 Cys Phe Phe Val
 65

<210> 75
 <211> 66
 <212> PRT
 <213> Mus musculus

<400> 75
 Tyr Glu Ala Arg Ile Val Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn
 1 5 10 15
 Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp
 20 25 30
 Lys Val Lys Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro
 35 40 45
 Ser Glu Asp Pro Trp Asp Gln His Ala Lys Cys Tyr Pro Gly Cys Lys
 50 55 60
 Tyr Leu
 65

<210> 76
 <211> 46
 <212> PRT
 <213> Mus musculus

<400> 76
 Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Ser Lys Ile Cys Met
 1 5 10 15
 Asp Arg Asn Ile Ala Ile Val Phe Phe Pro Cys Gly His Leu Ala Thr
 20 25 30
 Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
 35 40 45

001060 "E45960 09654743 090100

<210> 77
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 77
 Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
 1 5 10 15
 Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
 20 25 30
 Asn Asp Lys Val Lys Cys Phe Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45
 Lys Arg Gly Asp Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser
 50 55 60
 Cys Arg Phe Val
 65

<210> 78
 <211> 67
 <212> PRT
 <213> Homo sapiens

<400> 78
 Glu Asn Ala Arg Leu Leu Thr Phe Gln Thr Trp Pro Leu Thr Phe Leu
 1 5 10 15
 Ser Pro Thr Asp Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
 Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
 35 40 45
 Pro Lys Asp Asn Ala Met Ser Glu His Leu Arg His Phe Pro Lys Cys
 50 55 60
 Pro Phe Ile
 65

<210> 79
 <211> 68
 <212> PRT
 <213> Homo sapiens

<400> 79
 His Ala Ala Arg Phe Lys Thr Phe Phe Asn Trp Pro Ser Ser Val Leu
 1 5 10 15
 Val Asn Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn
 20 25 30
 Ser Asp Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp
 35 40 45
 Glu Ser Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg
 50 55 60
 Cys Glu Tyr Leu
 65

<210> 80
 <211> 46
 <212> PRT
 <213> Homo sapiens

<400> 80
 Glu Gln Leu Arg Arg Leu Pro Glu Glu Arg Thr Cys Lys Val Cys Met
 1 5 10 15
 Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val
 20 25 30
 Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
 35 40 45

<210> 81
 <211> 68
 <212> PRT
 <213> Mus musculus

<400> 81
 Glu Leu Tyr Arg Leu Ser Thr Tyr Ser Ala Phe Pro Arg Gly Val Pro
 1 5 10 15
 Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Ala
 20 25 30
 Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45
 Lys Gln Gly Asp Ser Pro Met Glu Lys His Arg Lys Leu Tyr Pro Ser
 50 55 60
 Cys Asn Phe Val
 65

<210> 82
 <211> 67
 <212> PRT
 <213> Mus musculus

<400> 82
 Glu Lys Ala Arg Leu Leu Thr Tyr Glu Thr Trp Pro Leu Ser Phe Leu
 1 5 10 15
 Ser Pro Ala Lys Leu Ala Lys Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
 Asp Arg Val Ala Cys Phe Ala Cys Asp Gly Lys Leu Ser Asn Trp Glu
 35 40 45
 Arg Lys Asp Asp Ala Met Ser Glu His Gln Arg His Phe Pro Ser Cys
 50 55 60
 Pro Phe Leu
 65

<210> 83
 <211> 68
 <212> PRT
 <213> Mus musculus

09654743 090100

001000" E445960

<400> 83

His Ala Ala Arg Ile Arg Thr Phe Ser Asn Trp Pro Ser Ser Ala Leu
 1 5 10 15
 Val His Ser Gln Glu Leu Ala Ser Ala Gly Phe Tyr Tyr Thr Gly His
 20 25 30
 Ser Asp Asp Val Lys Cys Leu Cys Cys Asp Gly Gly Leu Arg Cys Trp
 35 40 45
 Glu Ser Gly Asp Asp Pro Trp Val Glu His Ala Lys Trp Phe Pro Arg
 50 55 60
 Cys Glu Tyr Leu
 65

<210> 84

<211> 46

<212> PRT

<213> Mus musculus

<400> 84

Glu Gln Leu Arg Pro Leu Pro Glu Asp Arg Met Cys Lys Val Cys Met
 1 5 10 15
 Asp Arg Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val
 20 25 30
 Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
 35 40 45

<210> 85

<211> 68

<212> PRT

<213> Homo sapiens

<400> 85

Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
 1 5 10 15
 Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
 20 25 30
 Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45
 Lys Leu Gly Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser
 50 55 60
 Cys Ser Phe Ile
 65

<210> 86

<211> 67

<212> PRT

<213> Homo sapiens

SECRET

```
<210> 87
<211> 68
<212> PRT
<213> Homo sapiens
```

```
<210> 88
<211> 46
<212> PRT
<213> Homo sapiens
```

```
<210> 89
<211> 68
<212> PRT
<213> Mus musculus
```


001000 "CH2H960"

<400> 89

Glu	Leu	Tyr	Arg	Met	Ser	Thr	Tyr	Ser	Ala	Phe	Pro	Arg	Gly	Val	Pro
1				5					10					15	
Val	Ser	Glu	Arg	Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Val
			20					25					30		

Asn	Asp	Lys	Val	Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp
		35					40					45			
Lys	Gln	Gly	Asp	Ser	Pro	Val	Glu	Lys	His	Arg	Gln	Phe	Tyr	Pro	Ser
	50					55					60				
Cys	Ser	Phe	Val												
65															

<210> 90

<211> 67

<212> PRT

<213> Mus musculus

<400> 90

Glu	Glu	Ala	Arg	Phe	Leu	Thr	Tyr	Ser	Met	Trp	Pro	Leu	Ser	Phe	Leu
1				5					10					15	
Ser	Pro	Ala	Glu	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly
			20					25					30		
Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys	Gly	Gly	Lys	Leu	Ser	Asn	Trp	Glu
		35					40					45			
Pro	Lys	Asp	Tyr	Ala	Met	Ser	Glu	His	Arg	Arg	His	Phe	Pro	His	Cys
	50					55					60				
Pro	Phe	Leu													
65															

<210> 91

<211> 68

<212> PRT

<213> Mus musculus

<400> 91

His	Ser	Ala	Arg	Leu	Arg	Thr	Phe	Leu	Tyr	Trp	Pro	Pro	Ser	Val	Pro
1				5					10					15	
Val	Gln	Pro	Glu	Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Asp	Arg
			20					25					30		
Asn	Asp	Asp	Val	Lys	Cys	Leu	Cys	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp
		35					40					45			
Glu	Pro	Gly	Asp	Asp	Pro	Trp	Ile	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg
	50					55					60				
Cys	Glu	Phe	Leu												
65															

<210> 92

<211> 38

<212> PRT

<213> Mus musculus

<400> 92

Glu Arg Thr Cys Lys Val Cys Met Asp Arg Glu Val Ser Ile Val Phe

1

5

10

15

Ile Pro Cys Gly His Leu Val Val Cys Gln Glu Cys Ala Pro Ser Leu

20

25

30

Arg Lys Cys Pro Ile Cys

35

007060" E4245960

[illegible]

(1) GENERAL INFORMATION:

(i)-APPLICANT: Korneluk, Robert G.
Mackenzie, Alexander E.
Baird, Stephen

(ii) TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS, PROBES, AND DETECTION METHODS

(iii) NUMBER OF SEQUENCES: 42

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Fish & Richardson P.C.
(B) STREET: 225 Franklin Street
(C) CITY: Boston
(D) STATE: MA
(E) COUNTRY: USA
(F) ZIP: 02110-2804

(v) COMPUTER READABLE FORM:
 (A) MEDIUM TYPE: Floppy disk
 (B) COMPUTER: IBM PC compatible
 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER:
 (B) FILING DATE:
 (C) CLASSIFICATION:

(vi) CURRENT APPLICATION DATA:
 (A) APPLICATION NUMBER: US 08/511,485
 (B) FILING DATE: 04-AUG-1995
 (C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Clark, Paul T.
 (B) REGISTRATION NUMBER: 30,162
 (C) REFERENCE/DOCKET NUMBER: 07891/002001

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 617/542-5070
(B) TELEFAX: 617/542-8906
(C) TELEX: 200154

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(D) OTHER INFORMATION: Xaa at positons 2, 3, 4, 5,

6, 7, 9, 10, 11, 17, 18, 19, 20, 21, 23, 25, 30, 31, 32, 34, 35, 38, 39, 40, 41, 42, and 45 may be any amino acid. Xaa at position 8 is Glu or Asp. Xaa at positions 14 & 22 is Val or Ile.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

Glu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Lys Xaa Cys Met
1          5          10          15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Phe Xaa Pro Cys Gly His Xaa Xaa Xaa
20          25          30
Cys Xaa Xaa Cys Ala Xaa Xaa Xaa Xaa Xaa Cys Pro Xaa Cys
35          40          45

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa at positions 1, 2, 3, 6, 9, 10, 14, 15, 18, 19, 20, 21, 24, 30, 32, 33, 35, 37, 40, 42, 43, 44, 45, 46, 47, 49, 50, 51, 53, 54, 55, 56, 57, 59, 60, 61, 62, 64 and 66 may be any amino acid. Xaa at positions 13, 16 and 17 may be any amino acid or may be absent.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Xaa Xaa Xaa Arg Leu Xaa Thr Phe Xaa Xaa Trp Pro Xaa Xaa Xaa Xaa
1          5          10          15
Xaa Xaa Xaa Xaa Xaa Leu Ala Xaa Ala Gly Phe Tyr Tyr Xaa Gly Xaa
20          25          30
Xaa Asp Xaa Val Xaa Cys Phe Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Trp
35          40          45
Xaa Xaa Xaa Asp Xaa Xaa Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Pro Xaa
50          55          60
Cys Xaa Phe Val
65

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2540 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAAAGGTGG	ACAAAGTCCTA	TTTTCAAGAG	AAGATGACTT	TTAACAGTTT	TGAAGGATCT	60
AAAACTTG TG	TACCTGCAGA	CATCAATAAG	GAAGAAGAAT	TTGTAGAAGA	GTTTAATAGA	120
TTAAAACTT	TTGCTAATTT	TCCAAGTGGT	AGTCCTGTTT	CAGCATCAAC	ACTGGCACGA	180
GCAGGGTTTC	TTTATACTGG	TGAAGGAGAT	ACCGTGCGGT	GCTTTAGTTG	TCATGCAGCT	240
GTAGATAGAT	GGCAATATGG	AGACTCAGCA	GTTGGAAGAC	ACAGGAAAGT	ATCCCCAAAT	300
TGCAGATTTA	TCAACGGCTT	TTATCTTGAA	AATAGTGCCA	CGCAGTCTAC	AAATTCTGGT	360
ATCCAGAATG	GTCAGTACAA	AGTTGAAAAC	TATCTGGGAA	GCAGAGATCA	TTTTGCCTTA	420
GACAGGCCAT	CTGAGACACA	TGCAGACTAT	CTTTTGAGAA	CTGGGCAGGT	TGTAGATATA	480
TCAGACACCA	TATACCCGAG	GAACCCTGCC	ATGTATTGTG	AAGAAGCTAG	ATTAAAGTCC	540
TTTCAGAACT	GGCCAGACTA	TGCTCACCTA	ACCCCAAGAG	AGTTAGCAAG	TGCTGGACTC	600
TACTACACAG	GTATTGGTGA	CCAAGTGCAG	TGCTTTTGTT	GTGGTGGAAG	ACTGAAAAAT	660
TGGGAACCTT	GTGATCGTGC	CTGGTCAGAA	CACAGGCGAC	ACTTTCCTAA	TTGCTTCTTT	720
GTTTTGGGCC	GGAATCTTAA	TATTCGAAGT	GAATCTGATG	CTGTGAGTTC	TGATAGGAAT	780
TTCCCAAATT	CAACAAATCT	TCCAAGAAAT	CCATCCATGG	CAGATTATGA	AGCACGGATC	840
TTTACTTTTG	GGACATGGAT	ATACTCAGTT	AACAAGGAGC	AGCTTGCAAG	AGCTGGATTT	900
TATGCTTTAG	GTGAAGGTGA	TAAAGTAAAG	TGCTTTCACT	GTGGAGGAGG	GCTAACTGAT	960
TGGAAGCCCA	GTGAAGACCC	TTGGGAACAA	CATGCTAAAT	GGTATCCAGG	GTGCAAATAT	1020
CTGTTAGAAC	AGAAGGGACA	AGAATATATA	AACAATATTC	ATTAACTCA	TTCACTTGAG	1080
GAGTGTCTGG	TAAGAACTAC	TGAGAAAACA	CCATCACTAA	CTAGAAGAAT	TGATGATACC	1140
ATCTTCCAAA	ATCCTATGGT	ACAAGAAGCT	ATACGAATGG	GGTTCAGTTT	CAAGGACATT	1200
AAGAAAATAA	TGGAGGAAAA	AATTCAGATA	TCTGGGAGCA	ACTATAAATC	ACTTGAGGTT	1260
CTGGTTGCAG	ATCTAGTGAA	TGCTCAGAAA	GACAGTATGC	AAGATGAGTC	AAGTCAGACT	1320
TCATTACAGA	AAGAGATTAG	TACTGAAGAG	CAGCTAAGGC	GCCTGCAAGA	GGAGAAGCTT	1380
TGCAAAATCT	GTATGGATAG	AAATATTGCT	ATCGTTTTTG	TTCCTTGTGG	ACATCTAGTC	1440
ACTTGTAAC	AATGTGCTGA	AGCAGTTGAC	AAGTGTCCCA	TGTGCTACAC	AGTCATTACT	1500
TTCAAGCAAA	AAATTTTTAT	GTCTTAATCT	AACTCTATAG	TAGGCATGTT	ATGTTGTTCT	1560
TATTACCCTG	ATTGAATGTG	TGATGTGAAC	TGACTTTAAG	TAATCAGGAT	TGAATTCCAT	1620
TAGCATTTGC	TACCAAGTAG	GAAAAAAAT	GTACATGGCA	GTGTTTTAGT	TGGCAATATA	1680
ATCTTTGAAT	TTCTTGATTT	TTCAGGGTAT	TAGCTGTATT	ATCCATTTTT	TTTACTGTTA	1740

09654743.090100

TTTAATTGAA ACCATAGACT AAGAATAAGA AGCATCATAC TATAACTGAA CACAATGTGT	1800
ATTCATAGTA TACTGATTTA ATTTCTAAGT GTAAGTGAAT TAATCATCTG GATTTTTTAT	1860
TCTTTTCAGA TAGGCTTAAC AAATGGAGCT TTCTGTATAT AAATGTGGAG ATTAGAGTTA	1920
ATCTCCCCAA TCACATAATT TGTTTTGTGT GAAAAAGGAA TAAATTGTTT CATGCTGGTG	1980
GAAAGATAGA GATTGTTTTT AGAGGTTGGT TGTTGTGTTT TAGGATTCTG TCCATTTTCT	2040
TGTAAAGGGA TAAACACGGA CGTGTGCGAA ATATGTTTGT AAAGTGATTT GCCATTGTTG	2100
AAAGCGTATT TAATGATAGA ATACTATCGA GCCAACATGT ACTGACATGG AAAGATGTCA	2160
GAGATATGTT AAGTGTAATA TGCAAGTGGC GGGACACTAT GTATAGTCTG AGCCAGATCA	2220
AAGTATGTAT GTTGTTAATA TGCATAGAAC GAGAGATTTG GAAAGATATA CACCAAACCTG	2280
TTAAATGTGG TTTCTCTTCG GGGAGGGGGG GATTGGGGGA GGGGCCCCAG AGGGGTTTTA	2340
GAGGGGCCTT TTCACTTTCG ACTTTTTTCA TTTTGTTCCTG TTCGGATTTT TTATAAGTAT	2400
GTAGACCCCG AAGGGTTTTA TGGAACATAA CATCAGTAAC CTAACCCCG TGACTATCCT	2460
GTGCTCTTCC TAGGGAGCTG TGTTGTTTCC CACCCACCAC CCTTCCCTCT GAACAAATGC	2520
CTGAGTGCTG GGGCACTTTN	2540

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 497 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Phe	Asn	Ser	Phe	Glu	Gly	Ser	Lys	Thr	Cys	Val	Pro	Ala	Asp
1				5					10					15	
Ile	Asn	Lys	Glu	Glu	Glu	Phe	Val	Glu	Glu	Phe	Asn	Arg	Leu	Lys	Thr
		20						25					30		
Phe	Ala	Asn	Phe	Pro	Ser	Gly	Ser	Pro	Val	Ser	Ala	Ser	Thr	Leu	Ala
		35				40					45				
Arg	Ala	Gly	Phe	Leu	Tyr	Thr	Gly	Glu	Gly	Asp	Thr	Val	Arg	Cys	Phe
	50				55					60					
Ser	Cys	His	Ala	Ala	Val	Asp	Arg	Trp	Gln	Tyr	Gly	Asp	Ser	Ala	Val
65				70					75					80	
Gly	Arg	His	Arg	Lys	Val	Ser	Pro	Asn	Cys	Arg	Phe	Ile	Asn	Gly	Phe
			85					90					95		
Tyr	Leu	Glu	Asn	Ser	Ala	Thr	Gln	Ser	Thr	Asn	Ser	Gly	Ile	Gln	Asn

00654743-090100

100										105					110				
Gly	Gln	Tyr	Lys	Val	Glu	Asn	Tyr	Leu	Gly	Ser	Arg	Asp	His	Phe	Ala				
		115					120					125							
Leu	Asp	Arg	Pro	Ser	Glu	Thr	His	Ala	Asp	Tyr	Leu	Leu	Arg	Thr	Gly				
	130					135					140								
Gln	Val	Val	Asp	Ile	Ser	Asp	Thr	Ile	Tyr	Pro	Arg	Asn	Pro	Ala	Met				
145					150					155					160				
Tyr	Cys	Glu	Glu	Ala	Arg	Leu	Lys	Ser	Phe	Gln	Asn	Trp	Pro	Asp	Tyr				
				165					170					175					
Ala	His	Leu	Thr	Pro	Arg	Glu	Leu	Ala	Ser	Ala	Gly	Leu	Tyr	Tyr	Thr				
			180					185					190						
Gly	Ile	Gly	Asp	Gln	Val	Gln	Cys	Phe	Cys	Cys	Gly	Gly	Lys	Leu	Lys				
		195					200					205							
Asn	Trp	Glu	Pro	Cys	Asp	Arg	Ala	Trp	Ser	Glu	His	Arg	Arg	His	Phe				
	210					215					220								
Pro	Asn	Cys	Phe	Phe	Val	Leu	Gly	Arg	Asn	Leu	Asn	Ile	Arg	Ser	Glu				
225					230					235					240				
Ser	Asp	Ala	Val	Ser	Ser	Asp	Arg	Asn	Phe	Pro	Asn	Ser	Thr	Asn	Leu				
				245					250					255					
Pro	Arg	Asn	Pro	Ser	Met	Ala	Asp	Tyr	Glu	Ala	Arg	Ile	Phe	Thr	Phe				
			260					265					270						
Gly	Thr	Trp	Ile	Tyr	Ser	Val	Asn	Lys	Glu	Gln	Leu	Ala	Arg	Ala	Gly				
		275					280					285							
Phe	Tyr	Ala	Leu	Gly	Glu	Gly	Asp	Lys	Val	Lys	Cys	Phe	His	Cys	Gly				
	290					295					300								
Gly	Gly	Leu	Thr	Asp	Trp	Lys	Pro	Ser	Glu	Asp	Pro	Trp	Glu	Gln	His				
305					310					315					320				
Ala	Lys	Trp	Tyr	Pro	Gly	Cys	Lys	Tyr	Leu	Leu	Glu	Gln	Lys	Gly	Gln				
				325					330					335					
Glu	Tyr	Ile	Asn	Asn	Ile	His	Leu	Thr	His	Ser	Leu	Glu	Glu	Cys	Leu				
			340					345					350						
Val	Arg	Thr	Thr	Glu	Lys	Thr	Pro	Ser	Leu	Thr	Arg	Arg	Ile	Asp	Asp				
			355				360					365							
Thr	Ile	Phe	Gln	Asn	Pro	Met	Val	Gln	Glu	Ala	Ile	Arg	Met	Gly	Phe				
	370					375					380								
Ser	Phe	Lys	Asp	Ile	Lys	Lys	Ile	Met	Glu	Glu	Lys	Ile	Gln	Ile	Ser				
385					390					395					400				
Gly	Ser	Asn	Tyr	Lys	Ser	Leu	Glu	Val	Leu	Val	Ala	Asp	Leu	Val	Asn				
				405					410					415					
Ala	Gln	Lys	Asp	Ser	Met	Gln	Asp	Glu	Ser	Ser	Gln	Thr	Ser	Leu	Gln				
			420					425					430						

Lys Glu Ile Ser Thr Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys
 435 440 445

Leu Cys Lys Ile Cys Met Asp Arg Asn Ile Ala Ile Val Phe Val Pro
 450 455 460

Cys Gly His Leu Val Thr Cys Lys Gln Cys Ala Glu Ala Val Asp Lys
 465 470 475 480

Cys Pro Met Cys Tyr Thr Val Ile Thr Phe Lys Gln Lys Ile Phe Met
 485 490 495

Ser

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2676 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TCCTTGAGAT GTATCAGTAT AGGATTTAGG ATCTCCATGT TGGAAGTCTA AATGCATAGA	60
AATGGAAATA ATGGAAATTT TTCATTTTGG CTTTTCAGCC TAGTATTAAA ACTGATAAAA	120
GCAAAGCCAT GCACAAAACT ACCTCCCTAG AGAAAGGCTA GTCCCTTTTC TTCCCCATTC	180
ATTTTCATTAT GAACATAGTA GAAAACAGCA TATTCTTATC AAATTTGATG AAAAGCGCCA	240
ACACGTTTGA ACTGAAATAC GACTTGTCAT GTGAAGTCTA CCGAATGTCT ACGTATTCCA	300
CTTTTCCTGC TGGGGTTTCT GTCTCAGAAA GGAGTCTTGC TCGTGCTGGT TTCTATTACA	360
CTGGTGTGAA TGACAAGGTC AAATGCTTCT GTTGTGGCCT GATGCTGGAT AACTGGAAAA	420
GAGGAGACAG TCCTACTGAA AAGCATAAAA AGTTGTATCC TAGCTGCAGA TTCGTTTCTA	480
GTCTAAATTC CGTTAACAAC TTGGAAGCTA CCTCTCAGCC TACTTTTCCT TCTTCAGTAA	540
CACATTCCAC AACTCATTCT CTTCCGGGTA CAGAAAACAG TGGATATTTT CGTGGCTCTT	600
ATTCAAACTC TCCATCAAAT CCTGTAAACT CCAGAGCAAA TCAAGAATTT TCTGCCTTGA	660
TGAGAAGTTC CTACCCCTGT CCAATGAATA ACGAAAATGC CAGATTACTT ACTTTTCAGA	720
CATGGCCATT GACTTTTCTG TCGCCAACAG ATCTGGCAGC AGCAGGCTTT TACTACATAG	780
GACCTGGAGA CAGAGTGGCT TGCTTTGCCT GTGGTGAAA ATTGAGCAAT TGGGAACCGA	840
AGGATAATGC TATGTCAGAA CACCTGAGAC ATTTTCCCAA ATGCCCATTT ATAGAAAATC	900
AGCTTCAAGA CACTTCAAGA TACACAGTTT CTAATCTGAG CATGCAGACA CATGCAGCCC	960

GCTTTAAAAC	ATTCTTTAAC	TGGCCCTCTA	GTGTTCTAGT	TAATCCTGAG	CAGCTTGCAA	1020
GTGCGGGTTT	TTATTATGTG	GGTAACAGTG	ATGATGTCAA	ATGCTTTTGC	TGTGATGGTG	1080
GACTCAGGTG	TTGGGAATCT	GGAGATGATC	CATGGGTTCA	ACATGCCAAG	TGGTTTCCAA	1140
GGTGTGAGTA	CTTGATAAGA	ATTAAAGGAC	AGGAGTTCAT	CCGTCAAGTT	CAAGCCAGTT	1200
ACCCTCATCT	ACTTGAACAG	CTGCTATCCA	CATCAGACAG	CCCAGGAGAT	GAAAATGCAG	1260
AGTCATCAAT	TATCCATTTG	GAACCTGGAG	AAGACCATTG	AGAAGATGCA	ATCATGATGA	1320
ATACTCCTGT	GATTAATGCT	GCCGTGGAAA	TGGGCTTTAG	TAGAAGCCTG	GTAAAACAGA	1380
CAGTTCAGAG	AAAAATCCTA	GCAACTGGAG	AGAATTATAG	ACTAGTCAAT	GATCTTGTGT	1440
TAGACTTACT	CAATGCAGAA	GATGAAATAA	GGGAAGAGGA	GAGAGAAAGA	GCAACTGAGG	1500
AAAAAGAATC	AAATGATTTA	TTATTAATCC	GGAAGAATAG	AATGGCACTT	TTTCAACATT	1560
TGACTTGTGT	AATTCCAATC	CTGGATAGTC	TACTAACTGC	CGGAATTATT	AATGAACAAG	1620
AACATGATGT	TATTAAACAG	AAGACACAGA	CGTCTTTACA	AGCAAGAGAA	CTGATTGATA	1680
CGATTTTAGT	AAAAGGAAAT	ATTGCAGCCA	CTGTATTTCAG	AAACTCTCTG	CAAGAAGCTG	1740
AAGCTGTGTT	ATATGAGCAT	TTATTTGTGC	AACAGGACAT	AAAATATATT	CCCACAGAAG	1800
ATGTTTCAGA	TCTACCAAGT	GAAGAACAAT	TGCGGAGACT	ACCAGAAGAA	AGAACATGTA	1860
AAGTGTGTAT	GGACAAAGAA	GTGTCCATAG	TGTTTATTCC	TTGTGGTCAT	CTAGTAGTAT	1920
GCAAAGATTG	TGCTCCTTCT	TTAAGAAAGT	GTCTATTTG	TAGGAGTACA	ATCAAGGGTA	1980
CAGTTCGTAC	ATTTCTTTCA	TGAAGAAGAA	CCAAAACATC	GTCTAAACTT	TAGAATTAAT	2040
TTATTAAATG	TATTATAACT	TTAACTTTTA	TCCTAATTTG	GTTTCCTTAA	AATTTTTATT	2100
TATTTACAAC	TCAAAAAACA	TTGTTTTGTG	TAACATATTT	ATATATGTAT	CTAAACCATA	2160
TGAACATATA	TTTTTTAGAA	ACTAAGAGAA	TGATAGGCTT	TTGTTCTTAT	GAACGAAAAA	2220
GAGGTAGCAC	TACAAACACA	ATATTCAATC	CAAATTTTCAG	CATTATTGAA	ATTGTAAGTG	2280
AAGTAAAACT	TAAGATATTT	GAGTTAACCT	TTAAGAATTT	TAAATATTTT	GGCATTGTAC	2340
TAATACCGGG	AACATGAAGC	CAGGTGTGGT	GGTATGTACC	TGTAGTCCCA	GGCTGAGGCA	2400
AGAGAATTAC	TTGAGCCCAG	GAGTTTGAAT	CCATCCTGGG	CAGCATACTG	AGACCCTGCC	2460
TTTAAAAACN	AACAGNACCA	AANCCAAACA	CCAGGGACAC	ATTTCTCTGT	CTTTTTTGAT	2520
CAGTGTCCCTA	TACATCGAAG	GTGTGCATAT	ATGTTGAATC	ACATTTTAGG	GACATGGTGT	2580
TTTATAAAG	AATTCTGTGA	GNAAAAATTT	AATAAAGCAA	CCAAATTACT	CTTAAAAAAA	2640
AAAAAAAAAA	AAAAAACTCG	AGGGGCCCCG	ACCAAT			2676

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 604 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Asn	Ile	Val	Glu	Asn	Ser	Ile	Phe	Leu	Ser	Asn	Leu	Met	Lys	Ser	1	5	10	15
Ala	Asn	Thr	Phe	Glu	Leu	Lys	Tyr	Asp	Leu	Ser	Cys	Glu	Leu	Tyr	Arg	20	25	30	
Met	Ser	Thr	Tyr	Ser	Thr	Phe	Pro	Ala	Gly	Val	Pro	Val	Ser	Glu	Arg	35	40	45	
Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Val	Asn	Asp	Lys	Val	50	55	60	
Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Arg	Gly	Asp	65	70	75	80
Ser	Pro	Thr	Glu	Lys	His	Lys	Lys	Leu	Tyr	Pro	Ser	Cys	Arg	Phe	Val	85	90	95	
Gln	Ser	Leu	Asn	Ser	Val	Asn	Asn	Leu	Glu	Ala	Thr	Ser	Gln	Pro	Thr	100	105	110	
Phe	Pro	Ser	Ser	Val	Thr	His	Ser	Thr	His	Ser	Leu	Leu	Pro	Gly	Thr	115	120	125	
Glu	Asn	Ser	Gly	Tyr	Phe	Arg	Gly	Ser	Tyr	Ser	Asn	Ser	Pro	Ser	Asn	130	135	140	
Pro	Val	Asn	Ser	Arg	Ala	Asn	Gln	Glu	Phe	Ser	Ala	Leu	Met	Arg	Ser	145	150	155	160
Ser	Tyr	Pro	Cys	Pro	Met	Asn	Asn	Glu	Asn	Ala	Arg	Leu	Leu	Thr	Phe	165	170	175	
Gln	Thr	Trp	Pro	Leu	Thr	Phe	Leu	Ser	Pro	Thr	Asp	Leu	Ala	Arg	Ala	180	185	190	
Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys	195	200	205	
Gly	Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asn	Ala	Met	Ser	Glu	210	215	220	
His	Leu	Arg	His	Phe	Pro	Lys	Cys	Pro	Phe	Ile	Glu	Asn	Gln	Leu	Gln	225	230	235	240
Asp	Thr	Ser	Arg	Tyr	Thr	Val	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala	245	250	255	
Ala	Arg	Phe	Lys	Thr	Phe	Phe	Asn	Trp	Pro	Ser	Ser	Val	Leu	Val	Asn	260	265	270	

Pro Glu Gln Leu Ala Ser Ala Gly Phe Tyr Tyr Val Gly Asn Ser Asp
275 280 285

Asp Val Lys Cys Phe Cys Cys Asp Gly Gly Leu Arg Cys Trp Glu Ser
290 295 300

Gly Asp Asp Pro Trp Val Gln His Ala Lys Trp Phe Pro Arg Cys Glu
305 310 315 320

Tyr Leu Ile Arg Ile Lys Gly Gln Glu Phe Ile Arg Gln Val Gln Ala
325 330 335

Ser Tyr Pro His Leu Leu Glu Gln Leu Leu Ser Thr Ser Asp Ser Pro
340 345 350

Gly Asp Glu Asn Ala Glu Ser Ser Ile Ile His Leu Glu Pro Gly Glu
355 360 365

Asp His Ser Glu Asp Ala Ile Met Met Asn Thr Pro Val Ile Asn Ala
370 375 380

Ala Val Glu Met Gly Phe Ser Arg Ser Leu Val Lys Gln Thr Val Gln
385 390 395 400

Arg Lys Ile Leu Ala Thr Gly Glu Asn Tyr Arg Leu Val Asn Asp Leu
405 410 415

Val Leu Asp Leu Leu Asn Ala Glu Asp Glu Ile Arg Glu Glu Glu Arg
420 425 430

Glu Arg Ala Thr Glu Glu Lys Glu Ser Asn Asp Leu Leu Leu Ile Arg
435 440 445

Lys Asn Arg Met Ala Leu Phe Gln His Leu Thr Cys Val Ile Pro Ile
450 455 460

Leu Asp Ser Leu Leu Thr Ala Gly Ile Ile Asn Glu Gln Glu His Asp
465 470 475 480

Val Ile Lys Gln Lys Thr Gln Thr Ser Leu Gln Ala Arg Glu Leu Ile
485 490 495

Asp Thr Ile Leu Val Lys Gly Asn Ile Ala Ala Thr Val Phe Arg Asn
500 505 510

Ser Leu Gln Glu Ala Glu Ala Val Leu Tyr Glu His Leu Phe Val Gln
515 520 525

Gln Asp Ile Lys Tyr Ile Pro Thr Glu Asp Val Ser Asp Leu Pro Val
530 535 540

Glu Glu Gln Leu Arg Arg Leu Pro Glu Glu Arg Thr Cys Lys Val Cys
545 550 555 560

Met Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val
565 570 575

Val Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg
580 585 590

Ser Thr Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
595 600

00554743-090100

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTAGGTTACC TGAAAGAGTT ACTACAACCC CAAAGAGTTG TGTTCCTAAGT AGTATCTTGG 60
TAATTCAGAG AGATACTCAT CCTACCTGAA TATAAACTGA GATAAATCCA GTAAAGAAAG 120
TGTAGTAAAT TCTACATAAG AGTCTATCAT TGATTTCTTT TTGTGGTGGA AATCTTAGTT 180
CATGTGAAGA AATTTTCATGT GAATGTTTTA GCTATCAAAC AGTACTGTCA CCTACTCATG 240
CACAAAACCTG CCTCCCAAAG ACTTTTCCCA GGTCCCTCGT ATCAAAACAT TAAGAGTATA 300
ATGGAAGATA GCACGATCTT GTCAGATTGG ACAAACAGCA ACAAACAAAA AATGAAGTAT 360
GACTTTTCCT GTGAACTCTA CAGAATGTCT ACATATTCAA CTTTCCCCGC CGGGGTGCCT 420
GTCTCAGAAA GGAGTCTTGC TCGTGCTGGT TTTTATTATA CTGGTGTGAA TGACAAGGTC 480
AAATGCTTCT GTTGTGGCCT GATGCTGGAT AACTGGAAAC TAGGAGACAG TCCTATTCAA 540
AAGCATAAAC AGCTATATCC TAGCTGTAGC TTTATTGAGA ATCTGGTTTC AGCTAGTCTG 600
GGATCCACCT CTAAGAATAC GTCTCCAATG AGAAACAGTT TTGCACATTC ATTATCTCCC 660
ACCTTGGAAC ATAGTAGCTT GTTCAGTGGT TCTTACTCCA GCCTTCCTCC AAACCCTCTT 720
AATTCTAGAG CAGTTGAAGA CATCTCTTCA TCGAGGACTA ACCCCTACAG TTATGCAATG 780
AGTACTGAAG AAGCCAGATT TCTTACCTAC CATATGTGGC CATTAACTTT TTTGTCACCA 840
TCAGAATTGG CAAGAGCTGG TTTTATTAT ATAGGACCTG GAGATAGGGT AGCCTGCTTT 900
GCCTGTGGTG GGAAGCTCAG TAACTGGGAA CCAAGGATG ATGCTATGTC AGAACACCGG 960
AGGCATTTTC CCAACTGTCC ATTTTGGAA AATTCTCTAG AACTCTGAG GTTAGCATT 1020
TCAAATCTGA GCATGCAGAC ACATGCAGCT CGAATGAGAA CATTATATGTA CTGGCCATCT 1080
AGTGTTCCAG TTCAGCCTGA GCAGCTTGCA AGTGCTGGTT TTTATTATGT GGGTCGCAAT 1140
GATGATGTCA AATGCTTTGG TTGTGATGGT GGCTTGAGGT GTTGGGAATC TGGAGATGAT 1200
CCATGGGTAG AACATGCCAA GTGGTTTCCA AGGTGTGAGT TCTTGATACG AATGAAAGGC 1260
CAAGAGTTTG TTGATGAGAT TCAAGGTAGA TATCCTCATC TTCTGAACA GCTGTTGTCA 1320
ACTTCAGATA CCACTGGAGA AGAAAATGCT GACCCACCAA TTATTCATTT TGGACCTGGA 1380
GAAAGTTCTT CAGAAGATGC TGTCATGATG AATACACCTG TGGTTAAATC TGCCTTGGA 1440

ATGGGCTTTA ATAGAGACCT GGTGAAACAA ACAGTTCTAA GTAAATCCT GACAACTGGA 1500
GAGAACTATA AAACAGTTAA TGATATTGTG TCAGCACTTC TTAATGCTGA AGATGAAAAA 1560
AGAGAAGAGG AGAAGGAAAA ACAAGCTGAA GAAATGGCAT CAGATGATTT GTCATTAATT 1620
CGGAAGAACA GAATGGCTCT CTTTCAACAA TTGACATGTG TGCTTCCTAT CCTGGATAAT 1680
CTTTTAAAGG CCAATGTAAT TAATAAACAG GAACATGATA TTATTAAACA AAAAACACAG 1740
ATACCTTTAC AAGCGAGAGA ACTGATTGAT ACCATTGTTGGG TTAAAGGAAA TGCTGCGGCC 1800
AACATCTTCA AAAACTGTCT AAAAGAAATT GACTCTACAT TGTATAAGAA CTTATTTGTG 1860
GATAAGAATA TGAAGTATAT TCCAACAGAA GATGTTTCAG GTCTGTCACT GGAAGAACAA 1920
TTGAGGAGGT TGCAAGAAGA ACGAACTTGT AAAGTGTGTA TGGACAAAGA AGTTTCTGTT 1980
GTATTTATTC CTTGTGGTCA TCTGGTAGTA TGCCAGGAAT GTGCCCCCTC TCTAAGAAAA 2040
TGCCCTATTT GCAGGGGTAT AATCAAGGGT ACTGTTTCGTA CATTTCTCTC TTAAAGAAAA 2100
ATAGTCTATA TTTTAACCTG CATAAAAAGG TCTTTAAAT ATTGTTGAAC ACTTGAAGCC 2160
ATCTAAAGTA AAAAGGGAAT TATGAGTTTT TCAATTAGTA ACATTCATGT TCTAGTCTGC 2220
TTTGGTACTA ATAATCTTGT TTCTGAAAAG ATGGTATCAT ATATTTAATC TTAATCTGTT 2280
TATTTACAAG GGAAGATTTA TGTTTGGTGA ACTATATTAG TATGTATGTG TACCTAAGGG 2340
AGTAGCGTCN CTGCTTGTTA TGCATCATTT CAGGAGTTAC TGGATTTGTT GTTCTTTCAG 2400
AAAGCTTTGA ANACTAAATT ATAGTGTAGA AAAGAACTGG AAACCAGGAA CTCTGGAGTT 2460
CATCAGAGTT ATGGTGCCGA ATTGTCTTTG GTGCTTTTCA CTTGTGTTTT AAAATAAGGA 2520
TTTTTCTCTT ATTTCTCCCC CTAGTTTGTG AGAAACATCT CAATAAAGTG CTTTAAAAAG 2580

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 618 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met His Lys Thr Ala Ser Gln Arg Leu Phe Pro Gly Pro Ser Tyr Gln
1 5 10 15
Asn Ile Lys Ser Ile Met Glu Asp Ser Thr Ile Leu Ser Asp Trp Thr
20 25 30
Asn Ser Asn Lys Gln Lys Met Lys Tyr Asp Phe Ser Cys Glu Leu Tyr
35 40 45

001050" E45960

Arg	Met	Ser	Thr	Tyr	Ser	Thr	Phe	Pro	Ala	Gly	Val	Pro	Val	Ser	Glu	50	55	60
Arg	Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Val	Asn	Asp	Lys	65	70	75
Val	Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Leu	Gly	85	90	95
Asp	Ser	Pro	Ile	Gln	Lys	His	Lys	Gln	Leu	Tyr	Pro	Ser	Cys	Ser	Phe	100	105	110
Ile	Gln	Asn	Leu	Val	Ser	Ala	Ser	Leu	Gly	Ser	Thr	Ser	Lys	Asn	Thr	115	120	125
Ser	Pro	Met	Arg	Asn	Ser	Phe	Ala	His	Ser	Leu	Ser	Pro	Thr	Leu	Glu	130	135	140
His	Ser	Ser	Leu	Phe	Ser	Gly	Ser	Tyr	Ser	Ser	Leu	Pro	Pro	Asn	Pro	145	150	155
Leu	Asn	Ser	Arg	Ala	Val	Glu	Asp	Ile	Ser	Ser	Ser	Arg	Thr	Asn	Pro	165	170	175
Tyr	Ser	Tyr	Ala	Met	Ser	Thr	Glu	Glu	Ala	Arg	Phe	Leu	Thr	Tyr	His	180	185	190
Met	Trp	Pro	Leu	Thr	Phe	Leu	Ser	Pro	Ser	Glu	Leu	Ala	Arg	Ala	Gly	195	200	205
Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys	Gly	210	215	220
Gly	Lys	Leu	Ser	Asn	Trp	Glu	Pro	Lys	Asp	Asp	Ala	Met	Ser	Glu	His	225	230	235
Arg	Arg	His	Phe	Pro	Asn	Cys	Pro	Phe	Leu	Glu	Asn	Ser	Leu	Glu	Thr	245	250	255
Leu	Arg	Phe	Ser	Ile	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala	Ala	Arg	260	265	270
Met	Arg	Thr	Phe	Met	Tyr	Trp	Pro	Ser	Ser	Val	Pro	Val	Gln	Pro	Glu	275	280	285
Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Arg	Asn	Asp	Asp	Val	290	295	300
Lys	Cys	Phe	Gly	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser	Gly	Asp	305	310	315
Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu	Phe	Leu	325	330	335
Ile	Arg	Met	Lys	Gly	Gln	Glu	Phe	Val	Asp	Glu	Ile	Gln	Gly	Arg	Tyr	340	345	350
Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Thr	Thr	Gly	Glu	355	360	365
Glu	Asn	Ala	Asp	Pro	Pro	Ile	Ile	His	Phe	Gly	Pro	Gly	Glu	Ser	Ser	370	375	380

Ser Glu Asp Ala Val Met Met Asn Thr Pro Val Val Lys Ser Ala Leu
385 390 395 400

Glu Met Gly Phe Asn Arg Asp Leu Val Lys Gln Thr Val Leu Ser Lys
405 410 415

Ile Leu Thr Thr Gly Glu Asn Tyr Lys Thr Val Asn Asp Ile Val Ser
420 425 430

Ala Leu Leu Asn Ala Glu Asp Glu Lys Arg Glu Glu Glu Lys Glu Lys
435 440 445

Gln Ala Glu Glu Met Ala Ser Asp Asp Leu Ser Leu Ile Arg Lys Asn
450 455 460

Arg Met Ala Leu Phe Gln Gln Leu Thr Cys Val Leu Pro Ile Leu Asp
465 470 475 480

Asn Leu Leu Lys Ala Asn Val Ile Asn Lys Gln Glu His Asp Ile Ile
485 490 495

Lys Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg Glu Leu Ile Asp Thr
500 505 510

Ile Trp Val Lys Gly Asn Ala Ala Ala Asn Ile Phe Lys Asn Cys Leu
515 520 525

Lys Glu Ile Asp Ser Thr Leu Tyr Lys Asn Leu Phe Val Asp Lys Asn
530 535 540

Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly Leu Ser Leu Glu Glu
545 550 555 560

Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met Asp
565 570 575

Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val Cys
580 585 590

Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg Gly Ile
595 600 605

Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
610 615

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2100 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACACTCTGC TGGGCGGCGG GCCGCCCTCC TCCGGGACCT CCCCTCGGGA ACCGTCGCCC

60

GCGGCGCTTA	GTTAGGACTG	GAGTGCTTGG	CGCGAAAAGG	TGGACAAGTC	CTATTTTCCA	120
GAGAAGATGA	CTTTTAACAG	TTTTGAAGGA	ACTAGAACTT	TTGTACTTGC	AGACACCAAT	180
AAGGATGAAG	AATTTGTAGA	AGAGTTTAAT	AGATTAAAAA	CATTTGCTAA	CTTCCCAAGT	240
AGTAGTCCTG	TTTCAGCATC	AACATTGGCG	CGAGCTGGGT	TTCTTTTATAC	CGGTGAAGGA	300
GACACCGTGC	AATGTTTCAG	TTGTCATGCG	GCAATAGATA	GATGGCAGTA	TGGAGACTCA	360
GCTGTTGGAA	GACACAGGAG	AATATCCCCA	AATTGCAGAT	TTATCAATGG	TTTTTATTTT	420
GAAAATGGTG	CTGCACAGTC	TACAAATCCT	GGTATCCAAA	ATGGCCAGTA	CAAATCTGAA	480
AACTGTGTGG	GAAATAGAAA	TCCTTTTGCC	CCTGACAGGC	CACCTGAGAC	TCATGCTGAT	540
TATCTCTTGA	GAAGTGGACA	GGTTGTAGAT	ATTTTCAGACA	CCATATACCC	GAGGAACCCCT	600
GCCATGTGTA	GTGAAGAAGC	CAGATTGAAG	TCATTTCAGA	ACTGGCCGGA	CTATGCTCAT	660
TTAACCCCCA	GAGAGTTAGC	TAGTGCTGGC	CTCTACTACA	CAGGGGCTGA	TGATCAAGTG	720
CAATGCTTTT	GTTGTGGGGG	AAAAGTAAA	AATTGGGAAC	CCTGTGATCG	TGCCTGGTCA	780
GAACACAGGA	GACACTTTCC	CAATTGCTTT	TTTGTTTTGG	GCCGGAACGT	TAATGTTTCA	840
AGTGAATCTG	GTGTGAGTTC	TGATAGGAAT	TTCCCAAATT	CAACAAACTC	TCCAAGAAAT	900
CCAGCCATGG	CAGAATATGA	AGCACGGATC	GTTACTTTTG	GAACATGGAT	ATACTCAGTT	960
AACAAGGAGC	AGCTTGCAAG	AGCTGGATTT	TATGCTTTAG	GTGAAGGCCA	TAAAGTGAAG	1020
TGCTTCCACT	GTGGAGGAGG	GCTCACGGAT	TGGAAGCCAA	GTGAAGACCC	CTGGGACCAG	1080
CATGCTAAGT	GCTACCCAGG	GTGCAAATAC	CTATTGGATG	AGAAGGGGCA	AGAATATATA	1140
AATAATATTC	ATTTAACCCA	TCCACTTGAG	GAATCTTTGG	GAAGAACTGC	TGAAAAAACA	1200
CCACCGCTAA	CTAAAAAAAT	CGATGATACC	ATCTTCCAGA	ATCCTATGGT	GCAAGAAGCT	1260
ATACGAATGG	GATTTAGCTT	CAAGGACCTT	AAGAAAACAA	TGGAAGAAAA	AATCCAAACA	1320
TCCGGGAGCA	GCTATCTATC	ACTTGAGGTC	CTGATTGCAG	ATCTTGTGAG	TGCTCAGAAA	1380
GATAATACGG	AGGATGAGTC	AAGTCAAAC	TCATTGCAGA	AAGACATTAG	TACTGAAGAG	1440
CAGCTAAGGC	GCCTACAAGA	GGAGAAGCTT	TCCAAAATCT	GTATGGATAG	AAATATTGCT	1500
ATCGTTTTTT	TTCCTTGTGG	ACATCTGGCC	ACTTGTAAC	AGTGTGCAGA	AGCAGTTGAC	1560
AAATGTCCCA	TGTGCTACAC	CGTCATTACG	TTCAACCAAA	AAATTTTAT	GTCTTAGTGG	1620
GGCACCACAT	GTTATGTTCT	TCTTGCTCTA	ATTGAATGTG	TAATGGGAGC	GAACTTTAAG	1680
TAATCCTGCA	TTTGCAATCC	ATTAGCATCC	TGCTGTTTCC	AAATGGAGAC	CAATGCTAAC	1740
AGCACTGTTT	CCGTCTAAAC	ATTCAATTC	TGGATCTTTC	GAGTTATCAG	CTGTATCATT	1800
TAGCCAGTGT	TTTACTCGAT	TGAAACCTTA	GACAGAGAAG	CATTTTATAG	CTTTTCACAT	1860
GTATATTGGT	AGTACACTGA	CTTGATTCT	ATATGTAAGT	GAATTCATCA	CCTGCATGTT	1920

001060"EH245960

210	215	220
Pro Asn Cys Phe Phe Val Leu Gly Arg Asn Val Asn Val Arg Ser Glu		
225	230	235
Ser Gly Val Ser Ser Asp Arg Asn Phe Pro Asn Ser Thr Asn Ser Pro		
	245	250
Arg Asn Pro Ala Met Ala Glu Tyr Glu Ala Arg Ile Val Thr Phe Gly		
	260	265
Thr Trp Ile Tyr Ser Val Asn Lys Glu Gln Leu Ala Arg Ala Gly Phe		
	275	280
Tyr Ala Leu Gly Glu Gly Asp Lys Val Lys Cys Phe His Cys Gly Gly		
	290	295
Gly Leu Thr Asp Trp Lys Pro Ser Glu Asp Pro Trp Asp Gln His Ala		
305	310	315
Lys Cys Tyr Pro Gly Cys Lys Tyr Leu Leu Asp Glu Lys Gly Gln Glu		
	325	330
Tyr Ile Asn Asn Ile His Leu Thr His Pro Leu Glu Glu Ser Leu Gly		
	340	345
Arg Thr Ala Glu Lys Thr Pro Pro Leu Thr Lys Lys Ile Asp Asp Thr		
	355	360
Ile Phe Gln Asn Pro Met Val Gln Glu Ala Ile Arg Met Gly Phe Ser		
	370	375
Phe Lys Asp Leu Lys Lys Thr Met Glu Glu Lys Ile Gln Thr Ser Gly		
385	390	395
Ser Ser Tyr Leu Ser Leu Glu Val Leu Ile Ala Asp Leu Val Ser Ala		
	405	410
Gln Lys Asp Asn Thr Glu Asp Glu Ser Ser Gln Thr Ser Leu Gln Lys		
	420	425
Asp Ile Ser Thr Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu		
	435	440
Ser Lys Ile Cys Met Asp Arg Asn Ile Ala Ile Val Phe Phe Pro Cys		
	450	455
Gly His Leu Ala Thr Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys		
465	470	475
Pro Met Cys Tyr Thr Val Ile Thr Phe Asn Gln Lys Ile Phe Met Ser		
	485	490
		495

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Lys Ala Ala Arg Leu Gly Thr Tyr Thr Asn Trp Pro Val Gln Phe Leu
1 5 10 15
Glu Pro Ser Arg Met Ala Ala Ser Gly Phe Tyr Tyr Leu Gly Arg Gly
20 25 30
Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Thr Asn Trp Val
35 40 45
Arg Gly Asp Asp Pro Glu Thr Asp His Lys Arg Trp Ala Pro Gln Cys
50 55 60
Pro Phe Val
65

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 275 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Ser Asp Leu Arg Leu Glu Glu Val Arg Leu Asn Thr Phe Glu Lys
1 5 10 15
Trp Pro Val Ser Phe Leu Ser Pro Glu Thr Met Ala Lys Asn Gly Phe
20 25 30
Tyr Tyr Leu Gly Arg Ser Asp Glu Val Arg Cys Ala Phe Cys Lys Val
35 40 45
Glu Ile Met Arg Trp Lys Glu Gly Glu Asp Pro Ala Ala Asp His Lys
50 55 60
Lys Trp Ala Pro Gln Cys Pro Phe Val Lys Gly Ile Asp Val Cys Gly
65 70 75 80
Ser Ile Val Thr Thr Asn Asn Ile Gln Asn Thr Thr Thr His Asp Thr
85 90 95
Ile Ile Gly Pro Ala His Pro Lys Tyr Ala His Glu Ala Ala Arg Val
100 105 110
Lys Ser Phe His Asn Trp Pro Arg Cys Met Lys Gln Arg Pro Glu Gln
115 120 125
Met Ala Asp Ala Gly Phe Phe Tyr Thr Gly Tyr Gly Asp Asn Thr Lys

001060" E424560

130	135	140
Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp Glu Pro Glu Asp Val		
145	150	155 160
<hr/>		
Pro Trp Glu Gln His Val Arg Trp Phe Asp Arg Cys Ala Tyr Val Gln		
	165	170 175
Leu Val Lys Gly Arg Asp Tyr Val Gln Lys Val Ile Thr Glu Ala Cys		
	180	185 190
Val Leu Pro Gly Glu Asn Thr Thr Val Ser Thr Ala Ala Pro Val Ser		
	195	200 205
Glu Pro Ile Pro Glu Thr Lys Ile Glu Lys Glu Pro Gln Val Glu Asp		
	210	215 220
Ser Lys Leu Cys Lys Ile Cys Tyr Val Glu Glu Cys Ile Val Cys Phe		
	225	230 235 240
Val Pro Cys Gly His Val Val Ala Cys Ala Lys Cys Ala Leu Ser Val		
	245	250 255
Asp Lys Cys Pro Met Cys Arg Lys Ile Val Thr Ser Val Leu Lys Val		
	260	265 270
Tyr Phe Ser		
	275	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Thr Glu Leu Gly Met Glu Leu Glu Ser Val Arg Leu Ala Thr Phe	
1	5 10 15
Gly Glu Trp Pro Leu Asn Ala Pro Val Ser Ala Glu Asp Leu Val Ala	
	20 25 30
Asn Gly Phe Phe Ala Thr Gly Lys Trp Leu Glu Ala Glu Cys His Phe	
	35 40 45
Cys His Val Arg Ile Asp Arg Trp Glu Tyr Gly Asp Gln Val Ala Glu	
	50 55 60
Arg His Arg Arg Ser Ser Pro Ile Cys Ser Met Val Leu Ala Pro Asn	
	65 70 75 80
His Cys Gly Asn Val Pro Arg Ser Gln Glu Ser Asp Asn Glu Gly Asn	
	85 90 95

Ser Val Val Asp Ser Pro Glu Ser Cys Ser Cys Pro Asp Leu Leu Leu
100 105 110

Glu Ala Asn Arg Leu Val Thr Phe Lys Asp Trp Pro Asn Pro Asn Ile
115 120 125

Thr Pro Gln Ala Leu Ala Lys Ala Gly Phe Tyr Tyr Leu Asn Arg Leu
130 135 140

Asp His Val Lys Cys Val Trp Cys Asn Gly Val Ile Ala Lys Trp Glu
145 150 155 160

Lys Asn Asp Asn Ala Phe Glu Glu His Lys Arg Phe Phe Pro Gln Cys
165 170 175

Pro Arg Val Gln Met Gly Pro Leu Ile Glu Phe Ala Thr Gly Lys Asn
180 185 190

Leu Asp Glu Leu Gly Ile Gln Pro Thr Thr Leu Pro Leu Arg Pro Lys
195 200 205

Tyr Ala Cys Val Asp Ala Arg Leu Arg Thr Phe Thr Asp Trp Pro Ile
210 215 220

Ser Asn Ile Gln Pro Ala Ser Ala Leu Ala Gln Ala Gly Leu Tyr Tyr
225 230 235 240

Gln Lys Ile Gly Asp Gln Val Arg Cys Phe His Cys Asn Ile Gly Leu
245 250 255

Arg Ser Trp Gln Lys Glu Asp Glu Pro Trp Phe Glu His Ala Lys Trp
260 265 270

Ser Pro Lys Cys Gln Phe Val Leu Leu Ala Lys Gly Pro Ala Tyr Val
275 280 285

Ser Glu Val Leu Ala Thr Thr Ala Ala Asn Ala Ser Ser Gln Pro Ala
290 295 300

Thr Ala Pro Ala Pro Thr Leu Gln Ala Asp Val Leu Met Asp Glu Ala
305 310 315 320

Pro Ala Lys Glu Ala Leu Thr Leu Gly Ile Asp Gly Gly Val Val Arg
325 330 335

Asn Ala Ile Gln Arg Lys Leu Leu Ser Ser Gly Cys Ala Phe Ser Thr
340 345 350

Leu Asp Glu Leu Leu His Asp Ile Phe Asp Asp Ala Gly Ala Gly Ala
355 360 365

Ala Leu Glu Val Arg Glu Pro Pro Glu Pro Ser Ala Pro Phe Ile Glu
370 375 380

Pro Cys Gln Ala Thr Thr Ser Lys Ala Ala Ser Val Pro Ile Pro Val
385 390 395 400

Ala Asp Ser Ile Pro Ala Lys Pro Gln Ala Ala Glu Ala Val Ser Asn
405 410 415

Ile Ser Lys Ile Thr Asp Glu Ile Gln Lys Met Ser Val Ser Thr Pro
420 425 430

Asn Gly Asn Leu Ser Leu Glu Glu Glu Asn Arg Gln Leu Lys Asp Ala
 435 440 445

Arg Leu Cys Lys Val Cys Leu Asp Glu Glu Val Gly Val Val Phe Leu
 450 455 460

Pro Cys Gly His Leu Ala Thr Cys Asn Gln Cys Ala Pro Ser Val Ala
 465 470 475 480

Asn Cys Pro Met Cys Arg Ala Asp Ile Lys Gly Phe Val Arg Thr Phe
 485 490 495

Leu Ser

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Glu Glu Val Arg Leu Asn Thr Phe Glu Lys Trp Pro Val Ser Phe Leu
 1 5 10 15
 Ser Pro Glu Thr Met Ala Lys Asn Gly Phe Tyr Tyr Leu Gly Arg Ser
 20 25 30
 Asp Glu Val Arg Cys Ala Phe Cys Lys Val Glu Ile Met Arg Trp Lys
 35 40 45
 Glu Gly Glu Asp Pro Ala Ala Asp His Lys Lys Trp Ala Pro Gln Cys
 50 55 60
 Pro Phe Val
 65

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Ala Asn Arg Leu Val Thr Phe Lys Asp Trp Pro Asn Pro Asn Ile
 1 5 10 15

Thr Pro Gln Ala Leu Ala Lys Ala Gly Phe Tyr Tyr Leu Asn Arg Leu
 20 25 30

Asp His Val Lys Cys Val Trp Cys Asn Gly Val Ile Ala Lys Trp Glu
 35 40 45

Lys Asn Asp Asn Ala Phe Glu Glu His Lys Arg Phe Phe Pro Gln Cys
 50 55 60

Pro Arg Val
 65

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Ser Ser Pro
 1 5 10 15

Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
 20 25 30

Gly Asp Thr Val Gln Cys Phe Ser Cys His Ala Ala Ile Asp Arg Trp
 35 40 45

Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Arg Ile Ser Pro Asn
 50 55 60

Cys Arg Phe Ile
 65

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Glu Phe Asn Arg Leu Lys Thr Phe Ala Asn Phe Pro Ser Gly Ser Pro
 1 5 10 15

Val Ser Ala Ser Thr Leu Ala Arg Ala Gly Phe Leu Tyr Thr Gly Glu
 20 25 30

Gly Asp Thr Val Arg Cys Phe Ser Cys His Ala Ala Val Asp Arg Trp
 35 40 45

Gln Tyr Gly Asp Ser Ala Val Gly Arg His Arg Lys Val Ser Pro Asn
 50 55 60

Cys Arg Phe Ile
 65

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
 1 5 10 15

Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
 20 25 30

Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45

Lys Arg Gly Asp Ser Pro Thr Glu Lys His Lys Lys Leu Tyr Pro Ser
 50 55 60

Cys Arg Phe Val
 65

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Glu Leu Tyr Arg Met Ser Thr Tyr Ser Thr Phe Pro Ala Gly Val Pro
 1 5 10 15

Val Ser Glu Arg Ser Leu Ala Arg Ala Gly Phe Tyr Tyr Thr Gly Val
 20 25 30

Asn Asp Lys Val Lys Cys Phe Cys Cys Gly Leu Met Leu Asp Asn Trp
 35 40 45

Lys Leu Gly Asp Ser Pro Ile Gln Lys His Lys Gln Leu Tyr Pro Ser
 50 55 60
 Cys Ser Phe Ile
 65

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
 1 5 10 15
 Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ala
 20 25 30
 Asp Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
 35 40 45
 Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60
 Cys Phe Phe Val
 65

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Glu Glu Ala Arg Leu Lys Ser Phe Gln Asn Trp Pro Asp Tyr Ala His
 1 5 10 15
 Leu Thr Pro Arg Glu Leu Ala Ser Ala Gly Leu Tyr Tyr Thr Gly Ile
 20 25 30
 Gly Asp Gln Val Gln Cys Phe Cys Cys Gly Gly Lys Leu Lys Asn Trp
 35 40 45
 Glu Pro Cys Asp Arg Ala Trp Ser Glu His Arg Arg His Phe Pro Asn
 50 55 60

Cys Phe Phe Val
65

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Asn Ala Arg Leu Leu Thr Phe Gln Thr Trp Pro Leu Thr Phe Leu
1 5 10 15
Ser Pro Thr Asp Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
 35 40 45
Pro Lys Asp Asn Ala Met Ser Glu His Leu Arg His Phe Pro Lys Cys
 50 55 60
Pro Phe Ile
65

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 67 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Glu Glu Ala Arg Phe Leu Thr Tyr His Met Trp Pro Leu Thr Phe Leu
1 5 10 15
Ser Pro Ser Glu Leu Ala Arg Ala Gly Phe Tyr Tyr Ile Gly Pro Gly
 20 25 30
Asp Arg Val Ala Cys Phe Ala Cys Gly Gly Lys Leu Ser Asn Trp Glu
 35 40 45
Pro Lys Asp Asp Ala Met Ser Glu His Arg Arg His Phe Pro Asn Cys
 50 55 60
Pro Phe Leu
65

DECLASSIFICATION AUTHORITY

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

[illegible]

(i) SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```
Tyr Glu Ala Arg Ile Phe Thr Phe Gly Thr Trp Ile Tyr Ser Val Asn  
1          5           10         15  
  
Lys Glu Gln Leu Ala Arg Ala Gly Phe Tyr Ala Leu Gly Glu Gly Asp  
                20             25            30  
  
Lys Val Lys Cys Phe His Cys Gly Gly Gly Leu Thr Asp Trp Lys Pro  
      35              40  
  
Ser Glu Asp Pro Trp Glu Gln His Ala Lys Trp Tyr Pro Gly Cys Lys  
    50               55           60  
  
Tyr Leu.  
65
```

75

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

His	Ala	Ala	Arg	Phe	Lys	Thr	Phe	Phe	Asn	Trp	Pro	Ser	Ser	Val	Leu
1				5					10					15	
Val	Asn	Pro	Glu	Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Asn
			20					25					30		
Ser	Asp	Asp	Val	Lys	Cys	Phe	Cys	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp
			35				40					45			
Glu	Ser	Gly	Asp	Asp	Pro	Trp	Val	Gln	His	Ala	Lys	Trp	Phe	Pro	Arg
			50			55					60				
Cys	Glu	Tyr	Leu												
			65												

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not relevant
 (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

His	Ala	Ala	Arg	Met	Arg	Thr	Phe	Met	Tyr	Trp	Pro	Ser	Ser	Val	Pro
1				5					10					15	
Val	Gln	Pro	Glu	Gln	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Val	Gly	Arg
			20					25					30		
Asn	Asp	Asp	Val	Lys	Cys	Phe	Gly	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp
			35				40					45			
Glu	Ser	Gly	Asp	Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg
			50			55					60				
Cys	Glu	Phe	Leu												
			65												

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 68 amino acids

- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Glu Ala Ala Arg Leu Arg Thr Phe Ala Glu Trp Pro Arg Gly Leu Lys
1           5           10           15
Gln Arg Pro Glu Glu Leu Ala Glu Ala Gly Phe Phe Tyr Thr Gly Gln
          20           25           30
Gly Asp Lys Thr Arg Cys Phe Cys Cys Asp Gly Gly Leu Lys Asp Trp
          35           40           45
Glu Pro Asp Asp Ala Pro Trp Gln Gln His Ala Arg Trp Tyr Asp Arg
          50           55           60
Cys Glu Tyr Val
          65

```

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Glu Ala Ala Arg Val Lys Ser Phe His Asn Trp Pro Arg Cys Met Lys
1           5           10           15
Gln Arg Pro Glu Gln Met Ala Asp Ala Gly Phe Phe Tyr Thr Gly Tyr
          20           25           30
Gly Asp Asn Thr Lys Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp
          35           40           45
Glu Pro Glu Asp Val Pro Trp Glu Gln His Val Arg Trp Phe Asp Arg
          50           55           60
Cys Ala Tyr Val
          65

```

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant

(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Val Asp Ala Arg Leu Arg Thr Phe Thr Asp Trp Pro Ile Ser Asn Ile
1 5 10 15
Gln Pro Ala Ser Ala Leu Ala Gln Ala Gly Leu Tyr Tyr Gln Lys Ile
20 25 30
Gly Asp Gln Val Arg Cys Phe His Cys Asn Ile Gly Leu Arg Ser Trp
35 40 45
Gln Lys Glu Asp Glu Pro Trp Phe Glu His Ala Lys Trp Ser Pro Lys
50 55 60
Cys Gln Phe Val
65

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Glu Ser Val Arg Leu Ala Thr Phe Gly Glu Trp Pro Leu Asn Ala Pro
1 5 10 15
Val Ser Ala Glu Asp Leu Val Ala Asn Gly Phe Phe Gly Thr Trp Met
20 25 30
Glu Ala Glu Cys Asp Phe Cys His Val Arg Ile Asp Arg Trp Glu Tyr
35 40 45
Gly Asp Leu Val Ala Glu Arg His Arg Arg Ser Ser Pro Ile Cys Ser
50 55 60
Met Val
65

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

SECRET

Glu Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys Lys Val Cys Met
 1 5 10 15
 Asp Lys Glu Val Ser Val Val Phe Ile Pro Cys Gly His Leu Val Val
 20 25 30
 Cys Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
 35 40 45

(i) **SEQUENCE CHARACTERISTICS:**
 (A) **LENGTH:** 46 amino acids
 (B) **TYPE:** amino acid
 (C) **STRANDEDNESS:** not relevant
 (D) **TOPOLOGY:** both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Glu Gln Leu Arg Arg Leu Pro Glu Glu Arg Thr Cys Lys Val Cys Met
1 5 10 15

Asp Lys Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val
20 25 30

Cys Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys
35 40 45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: both

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Ser Lys Ile Cys Met
 1 5 10 15
 Asp Arg Asn Ile Ala Ile Val Phe Phe Pro Cys Gly His Leu Ala Thr
 20 25 30
 Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys

45

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
(B) ~~TYPE: amino acid~~
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Glu Gln Leu Arg Arg Leu Gln Glu Glu Lys Leu Cys Lys Ile Cys Met
1 5 10 15

Asp Arg Asn Ile Ala Ile Val Phe Val Pro Cys Gly His Leu Val Thr
20 25 30

Cys Lys Gln Cys Ala Glu Ala Val Asp Lys Cys Pro Met Cys
35 40 45

(2) INFORMATION FOR SEO ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Glu Glu Asn Arg Gln Leu Lys Asp Ala Arg Leu Cys Lys Val Cys Leu
1 5 10 15

Asp Glu Glu Val Gly Val Val Phe Leu Pro Cys Gly His Leu Ala Thr
20 25 30

Cys Asn Gln Cys Ala Pro Ser Val Ala Asn Cys Pro Met Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

SECRET

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Lys Glu Pro Gln Val Glu Asp Ser Lys Leu Cys Lys Ile Cys Tyr
1 5 10 15
Val Glu Glu Cys Ile Val Cys Phe Val Pro Cys Gly His Val Val Ala
20 25 30
Cys Ala Lys Cys Ala Leu Ser Val Asp Lys Cys Pro Met Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 46 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: not relevant
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ala Val Glu Ala Glu Val Ala Asp Asp Arg Leu Cys Lys Ile Cys Leu
1 5 10 15
Gly Ala Glu Lys Thr Val Cys Phe Val Pro Cys Gly His Val Val Ala
20 25 30
Cys Gly Lys Cys Ala Ala Gly Val Thr Thr Cys Pro Val Cys
35 40 45

(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2474 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAATTCCGGG AGACCTACAC CCCCGGAGAT CAGAGGTCAT TGCTGGCGTT CAGAGCCTAG 60
GAAGTGGGCT GCGGTATCAG CCTAGCAGTA AAACCGACCA GAAGCCATGC ACAA AACTAC 120
ATCCCCAGAG AAAGACTTGT CCCTTCCCCT CCCTGTCATC TCACCATGAA CATGGTTCAA 180
GACAGCGCCT TTCTAGCCAA GCTGATGAAG AGTGCTGACA CCTTTGAGTT GAAGTATGAC 240
TTTCCTGTG AGCTGTACCG ATTGTCCACG TATTCAGCTT TTCCCAGGGG AGTTCCTGTG 300
TCAGAAAGGA GTCTGGCTCG TGCTGGCTTT TACTACACTG GTGCCAATGA CAAGGTCAAG 360

09654743 "090100

TGCTTCTGCT	GTGGCCTGAT	GCTAGACAAC	TGGAAACAAG	GGGACAGTCC	CATGGAGAAG	420
CACAGAAAGT	TGTACCCCAG	CTGCAACTTT	GTACAGACTT	TGAATCCAGC	CAACAGTCTG	480
GAAGCTAGTC	CTCGGCCTTC	TCTTCCTTCC	ACGGCGATGA	GCACCATGCC	TTTGAGCTTT	540
GCAAGTTCTG	AGAATACTGG	CTATTTTCAGT	GGCTCTTACT	CGAGCTTTCC	CTCAGACCCT	600
GTGAACTTCC	GAGCAAATCA	AGATTGTCCT	GCTTTGAGCA	CAAGTCCCTA	CCACTTTGCA	660
ATGAACACAG	AGAAGGCCAG	ATTACTCACC	TATGAAACAT	GGCCATTGTC	TTTTCTGTCA	720
CCAGCAAAGC	TGGCCAAAGC	AGGCTTCTAC	TACATAGGAC	CTGGAGATAG	AGTGGCCTGC	780
TTTGCCTGCG	ATGGGAAACT	GAGCAACTGG	GAACGTAAAG	ATGATGCTAT	GTCAGAGCAC	840
CAGAGGCATT	TCCCCAGCTG	TCCGTTCTTA	AAAGACTTGG	GTCAGTCTGC	TTCGAGATAC	900
ACTGTCTCTA	ACCTGAGCAT	GCAGACACAC	GCAGCCCGTA	TTAGAACATT	CTCTAACTGG	960
CCTTCTAGTG	CACTAGTTCA	TTCCAGGAA	CTTGCAAGTG	CGGGCTTTTA	TTATACAGGA	1020
CACAGTGATG	ATGTCAAGTG	TTTATGCTGT	GATGGTGGGC	TGAGGTGCTG	GGAATCTGGA	1080
GATGACCCCT	GGGTGGAACA	TGCCAAGTGG	TTTCCAAGGT	GTGAGTACTT	GCTCAGAATC	1140
AAAGGCCAAG	AATTTGTCAG	CCAAGTTCAA	GCTGGCTATC	CTCATCTACT	TGAGCAGCTA	1200
TTATCTACGT	CAGACTCCCC	AGAAGATGAG	AATGCAGACG	CAGCAATCGT	GCATTTTGGC	1260
CCTGGAGAAA	GTTGGAAGA	TGTCGTCATG	ATGAGCACGC	CTGTGGTTAA	AGCAGCCTTG	1320
GAAATGGGCT	TCAGTAGGAG	CCTGGTGAGA	CAGACGGTTC	AGTGGCAGAT	CCTGGCCACT	1380
GGTGAGAACT	ACAGGACCGT	CAGTGACCTC	GTTATAGGCT	TACTCGATGC	AGAAGACGAG	1440
ATGAGAGAGG	AGCAGATGGA	GCAGGCGGCC	GAGGAGGAGG	AGTCAGATGA	TCTAGCACTA	1500
ATCCGGAAGA	ACAAAATGGT	GCTTTTCCAA	CATTTGACGT	GTGTGACACC	AATGCTGTAT	1560
TGCCTCCTAA	GTGCAAGGGC	CATCACTGAA	CAGGAGTGCA	ATGCTGTGAA	ACAGAAACCA	1620
CACACCTTAC	AAGCAAGCAC	ACTGATTGAT	ACTGTGTTAG	CAAAAGGAAA	CACTGCAGCA	1680
ACCTCATTCA	GAAACTCCCT	TCGGGAAATT	GACCCTGCGT	TATACAGAGA	TATATTTGTG	1740
CAACAGGACA	TTAGGAGTCT	TCCCACAGAT	GACATTGCAG	CTCTACCAAT	GGAAGAACAG	1800
TTGCGGCCCC	TCCCGGAGGA	CAGAATGTGT	AAAGTGTGTA	TGGACCGAGA	GGTATCCATC	1860
GTGTTCATTC	CCTGTGGCCA	TCTGGTCTGT	TGCAAAGACT	GCGCTCCCTC	TCTGAGGAAG	1920
TGTCCCATCT	GTAGAGGGAC	CATCAAGGGC	ACAGTGCGCA	CATTTCTCTC	CTGAACAAGA	1980
CTAATGGTCC	ATGGCTGCAA	CTTCAGCCAG	GAGGAAGTTC	ACTGTCACTC	CCAGTTCCAT	2040
TCGGAACCTG	AGGCCAGCCT	GGATAGCACG	AGACACCGCC	AAACACACAA	ATATAAACAT	2100
GAAAACTTT	TGTCTGAAGT	CAAGAATGAA	TGAATTACTT	ATATAATAAT	TTAATTGGT	2160
TTCTTAAAA	GTGCTATTTG	TTCCCAACTC	AGAAAATTGT	TTTCTGTAAA	CATATTTACA	2220

TACTACCTGC ATCTAAAGTA TTCATATATT CATATATTCA GATGTCATGA GAGAGGGTTT 2280
 TGTTCCTTGGT CCTGAAAAGC TGGTTTATCA TCTGATCAGC ATATACTGCG CAACGGGCAG 2340
 GGCTAGAATC CATGAACCAA GCTGCAAAGA TCTCACGCTA AATAAGGCCG AAAGATTGG 2400
 AGAAACGAAA GGAAATTCTT TCCTGTCCAA TGTATACTCT TCAGACTAAT GACCTCTTCC 2460
 TATCAAGCCT TCTA 2474

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 602 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Met	Asn	Met	Val	Gln	Asp	Ser	Ala	Phe	Leu	Ala	Lys	Leu	Met	Lys	Ser	1	5	10	15
Ala	Asp	Thr	Phe	Glu	Leu	Lys	Tyr	Asp	Phe	Ser	Cys	Glu	Leu	Tyr	Arg	20	25	30	
Leu	Ser	Thr	Tyr	Ser	Ala	Phe	Pro	Arg	Gly	Val	Pro	Val	Ser	Glu	Arg	35	40	45	
Ser	Leu	Ala	Arg	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	Ala	Asn	Asp	Lys	Val	50	55	60	
Lys	Cys	Phe	Cys	Cys	Gly	Leu	Met	Leu	Asp	Asn	Trp	Lys	Gln	Gly	Asp	65	70	75	80
Ser	Pro	Met	Glu	Lys	His	Arg	Lys	Leu	Tyr	Pro	Ser	Cys	Asn	Phe	Val	85	90	95	
Gln	Thr	Leu	Asn	Pro	Ala	Asn	Ser	Leu	Glu	Ala	Ser	Pro	Arg	Pro	Ser	100	105	110	
Leu	Pro	Ser	Thr	Ala	Met	Ser	Thr	Met	Pro	Leu	Ser	Phe	Ala	Ser	Ser	115	120	125	
Glu	Asn	Thr	Gly	Tyr	Phe	Ser	Gly	Ser	Tyr	Ser	Ser	Phe	Pro	Ser	Asp	130	135	140	
Pro	Val	Asn	Phe	Arg	Ala	Asn	Gln	Asp	Cys	Pro	Ala	Leu	Ser	Thr	Ser	145	150	155	160
Pro	Tyr	His	Phe	Ala	Met	Asn	Thr	Glu	Lys	Ala	Arg	Leu	Leu	Thr	Tyr	165	170	175	
Glu	Thr	Trp	Pro	Leu	Ser	Phe	Leu	Ser	Pro	Ala	Lys	Leu	Ala	Lys	Ala	180	185	190	
Gly	Phe	Tyr	Tyr	Ile	Gly	Pro	Gly	Asp	Arg	Val	Ala	Cys	Phe	Ala	Cys				

195					200					205					
Asp	Gly	Lys	Leu	Ser	Asn	Trp	Glu	Arg	Lys	Asp	Asp	Ala	Met	Ser	Glu
	210					215					220				
His	Gln	Arg	His	Phe	Pro	Ser	Cys	Pro	Phe	Leu	Lys	Asp	Leu	Gly	Gln
225					230					235					240
Ser	Ala	Ser	Arg	Tyr	Thr	Val	Ser	Asn	Leu	Ser	Met	Gln	Thr	His	Ala
				245					250					255	
Ala	Arg	Ile	Arg	Thr	Phe	Ser	Asn	Trp	Pro	Ser	Ser	Ala	Leu	Val	His
			260					265					270		
Ser	Gln	Glu	Leu	Ala	Ser	Ala	Gly	Phe	Tyr	Tyr	Thr	Gly	His	Ser	Asp
		275					280					285			
Asp	Val	Lys	Cys	Leu	Cys	Cys	Asp	Gly	Gly	Leu	Arg	Cys	Trp	Glu	Ser
	290					295					300				
Gly	Asp	Asp	Pro	Trp	Val	Glu	His	Ala	Lys	Trp	Phe	Pro	Arg	Cys	Glu
305					310					315					320
Tyr	Leu	Leu	Arg	Ile	Lys	Gly	Gln	Glu	Phe	Val	Ser	Gln	Val	Gln	Ala
				325					330					335	
Gly	Tyr	Pro	His	Leu	Leu	Glu	Gln	Leu	Leu	Ser	Thr	Ser	Asp	Ser	Pro
			340					345					350		
Glu	Asp	Glu	Asn	Ala	Asp	Ala	Ala	Ile	Val	His	Phe	Gly	Pro	Gly	Glu
		355					360					365			
Ser	Ser	Glu	Asp	Val	Val	Met	Met	Ser	Thr	Pro	Val	Val	Lys	Ala	Ala
		370					375				380				
Leu	Glu	Met	Gly	Phe	Ser	Arg	Ser	Leu	Val	Arg	Gln	Thr	Val	Gln	Trp
385					390					395					400
Gln	Ile	Leu	Ala	Thr	Gly	Glu	Asn	Tyr	Arg	Thr	Val	Ser	Asp	Leu	Val
				405					410					415	
Ile	Gly	Leu	Leu	Asp	Ala	Glu	Asp	Glu	Met	Arg	Glu	Glu	Gln	Met	Glu
			420					425					430		
Gln	Ala	Ala	Glu	Glu	Glu	Glu	Ser	Asp	Asp	Leu	Ala	Leu	Ile	Arg	Lys
		435					440					445			
Asn	Lys	Met	Val	Leu	Phe	Gln	His	Leu	Thr	Cys	Val	Thr	Pro	Met	Leu
		450				455					460				
Tyr	Cys	Leu	Leu	Ser	Ala	Arg	Ala	Ile	Thr	Glu	Gln	Glu	Cys	Asn	Ala
465					470					475					480
Val	Lys	Gln	Lys	Pro	His	Thr	Leu	Gln	Ala	Ser	Thr	Leu	Ile	Asp	Thr
				485					490					495	
Val	Leu	Ala	Lys	Gly	Asn	Thr	Ala	Ala	Thr	Ser	Phe	Arg	Asn	Ser	Leu
			500					505					510		
Arg	Glu	Ile	Asp	Pro	Ala	Leu	Tyr	Arg	Asp	Ile	Phe	Val	Gln	Gln	Asp
		515					520					525			

Ile Arg Ser Leu Pro Thr Asp Asp Ile Ala Ala Leu Pro Met Glu Glu
530 535 540

Gln Leu Arg Pro Leu Pro Glu Asp Arg Met Cys Lys Val Cys Met Asp
545 550 555 560

Arg Glu Val Ser Ile Val Phe Ile Pro Cys Gly His Leu Val Val Cys
565 570 575

Lys Asp Cys Ala Pro Ser Leu Arg Lys Cys Pro Ile Cys Arg Gly Thr
580 585 590

Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
595 600

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CTGTGGTGGG	GATCTATTGT	CCAAGTGGTG	AGAAACTTCA	TCTGGAAGTT	TAAGCGGTCA	60
GAAATACTAT	TACTACTCAT	GGACAAACT	GTCTCCAGA	GA CTGCCCCA	AGGTACCTTA	120
CACCCAAAAA	CTTAAACGTA	TAATGGAGAA	GAGCACAATC	TTGTCAAATT	GGACAAAGGA	180
GAGCGAAGAA	AAAATGAAGT	TTGACTTTTC	GTGTGAACTC	TACCGAATGT	CTACATATTC	240
AGCTTTTCCC	AGGGGAGTTC	CTGTCTCAGA	GAGGAGTCTG	GCTCGTGCTG	GCTTTTATTA	300
TACAGGTGTG	AATGACAAAG	TCAAGTGCTT	CTGCTGTGGC	CTGATGTTGG	ATAACTGGAA	360
ACAAGGGGAC	AGTCCTGTTG	AAAAGCACAG	ACAGTTCTAT	CCCAGCTGCA	GCTTTGTACA	420
GACTCTGCTT	TCAGCCAGTC	TGCAGTCTCC	ATCTAAGAAT	ATGTCTCCTG	TGAAAAGTAG	480
ATTTGCACAT	TCGTACCTC	TGGAACGAGG	TGGCATTAC	TCCAACCTGT	GCTCTAGCCC	540
TCTTAATTCT	AGAGCAGTGG	AAGACTTCTC	ATCAAGGATG	GATCCCTGCA	GCTATGCCAT	600
GAGTACAGAA	GAGGCCAGAT	TTCTTACTTA	CAGTATGTGG	CCTTTAAGTT	TTCTGTCAAC	660
AGCAGAGCTG	GCCAGAGCTG	GCTTCTATTA	CATAGGGCCT	GGAGACAGGG	TGGCCTGTTT	720
TGCCTGTGGT	GGGAACTGA	GCAACTGGGA	ACCAAAGGAT	TATGCTATGT	CAGAGCACCG	780
CAGACATTTT	CCCCACTGTC	CATTTCTGGA	AAATACTTCA	GAAACACAGA	GGTTTAGTAT	840
ATCAAATCTA	AGTATGCAGA	CACACTCTGC	TCGATTGAGG	ACATTTCTGT	ACTGGCCACC	900
TAGTGTTCCT	GTTCAGCCCC	AGCAGCTTGC	AAGTGCTGGA	TTCTATTACG	TGGATCGCAA	960

TGATGATGTC	AAGTGCCTTT	GTTGTGATGG	TGGCTTGAGA	TGTTGGGAAC	CTGGAGATGA	1020	
CCCCTGGATA	GAACACGCCA	AATGGTTTCC	AAGGTGTGAG	TTCTTGATAC	GGATGAAGGG	1080	
TCAGGAGTTT	GTTGATGAGA	TTCAAGCTAG	ATATCCTCAT	CTTCTTGAGC	AGCTGTTGTC	1140	
CACTTCAGAC	ACCCCAGGAG	AAGAAAATGC	TGAGCCTACA	GAGACAGTGG	TGCATTTTGG	1200	
CCCTGGAGAA	AGTTCGAAAG	ATGTCGTCAT	GATGAGCACG	CCTGTGGTTA	AAGCAGCCTT	1260	
GGAAATGGGC	TTCAGTAGGA	GCCTGGTGAG	ACAGACGGTT	CAGCGGCAGA	TCCTGGCCAC	1320	
TGGTGAGAAC	TACAGGACCG	TCAATGATAT	TGTCTCAGTA	CTTTTGAATG	CTGAAGATGA	1380	
GAGAAGAGAA	GAGGAGAAGG	AAAGACAGAC	TGAAGAGATG	GCATCAGGTG	ACTTATCACT	1440	
GATTTCGGAAG	AATAGAATGG	CCCTCTTTCA	ACAGTTGACA	CATGTCCTTC	CTATCCTGGA	1500	
TAATCTTCTT	GAGGCCAGTG	TAATTACAAA	ACAGGAACAT	GATATTATTA	GACAGAAAAC	1560	
ACAGATACCC	TTACAAGCAA	GAGAGCTTAT	TGACACCGTT	TTAGTCAAGG	GAAATGCTGC	1620	
AGCCAACATC	TTCAAAAAC	CTCTGAAGGG	AATTGACTCC	ACGTTATATG	AAAACCTATT	1680	
TGTGGAAAAG	AATATGAAGT	ATATTCCAAC	AGAAGACGTT	TCAGGCTTGT	CATTGGAAGA	1740	
GCAGTTGCGG	AGATTACAAG	AAGAACGAAC	TTGCAAAGTG	TGTATGGACA	GAGAGGTTTC	1800	
TATTGTGTTC	ATTCCGTGTG	GTCATCTAGT	AGTCTGCCAG	GAATGTGCCC	CTTCTCTAAG	1860	
GAAGTGCCCC	ATCTGCAGGG	GGACAATCAA	GGGGACTGTG	CGCACATTTT	TCTCATGAGT	1920	
GAAGAATGGT	CTGAAAGTAT	TGTTGGACAT	CAGAAGCTGT	CAGAACAAAG	AATGAACTAC	1980	
TGATTTCAGC	TCTTCAGCAG	GACATTCTAC	TCTCTTTCAA	GATTAGTAAT	CTTGCTTTAT	2040	
GAAGGGTAGC	ATTGTATATT	TAAGCTTAGT	CTGTTGCAAG	GGAAGGTCTA	TGCTGTTGAG	2100	
CTACAGGACT	GTGTCTGTTC	CAGAGCAGGA	GTTGGGATGC	TTGCTGTATG	TCCTTCAGGA	2160	
CTTCTTGGGA	TTTGGGAATT	TGGGGAAAGC	TTTGGGAATCC	AGTGATGTGG	AGCTCAGAAA	2220	
TCCTGGAACC	AGTGA	CTCTG	GTACTCAGTA	GATAGGGTAC	CCTGTACTTC	TTGGTGCTTT	2280
TCCAGTCTGG	GAAATAAGGA	GGAATCTGCT	GCTGGTAAAA	ATTTGCTGGA	TGTGAGAAAT	2340	
AGATGAAAGT	GTTTCGGGTG	GGGGCGTGCA	TCAGTGTAGT	GTGTGCAGGG	ATGTATGCAG	2400	
GCCAAACACT	GTGTAG					2416	

- (2) INFORMATION FOR SEQ ID NO:42:

THE CHINESE

87

Thr Pro Gly Glu Glu Asn Ala Asp Pro Thr Glu Thr Val Val His Phe
340 345 350

Val Lys Ala Ala Leu Glu Met Gly Phe Ser Arg Ser Leu Val Arg Gln
370 375 380

Asn Asp Ile Val Ser Val Leu Leu Asn Ala Glu Asp Glu Arg Arg Glu
405 410 415

Glu Glu Lys Glu Arg Gln Thr Glu Glu Met Ala Ser Gly Asp Leu Ser
420 425 430

Leu Ile Arg Lys Asn Arg Met Ala Leu Phe Gln Gln Leu Thr His Val
435 440 445

Leu Pro Ile Leu Asp Asn Leu Leu Glu Ala Ser Val Ile Thr Lys Gln
450 455 460

Glu His Asp Ile Ile Arg Gln Lys Thr Gln Ile Pro Leu Gln Ala Arg
465 470 475 480

Glu Leu Ile Asp Thr Val Leu Val Lys Gly Asn Ala Ala Ala Asn Ile
485 490 495

Phe Lys Asn Ser Leu Lys Gly Ile Asp Ser Thr Leu Tyr Glu Asn Leu
500 505 510

Phe Val Glu Lys Asn Met Lys Tyr Ile Pro Thr Glu Asp Val Ser Gly
515 520 525

Leu Ser Leu Glu Glu Gln Leu Arg Arg Leu Gln Glu Glu Arg Thr Cys
530 535 540

Lys Val Cys Met Asp Arg Glu Val Ser Ile Val Phe Ile Pro Cys Gly
545 550 555 560

His Leu Val Val Cys Gln Glu Cys Ala Pro Ser Leu Arg Lys Cys Pro
565 570 575

Ile Cys Arg Gly Thr Ile Lys Gly Thr Val Arg Thr Phe Leu Ser
580 585 590